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Lys Glu Tyr Thr Asp Ile Thr Tyr Lys Gln Leu Asn Lys Met Arg Asp
 435 440 445
 Arg Tyr Ser Leu Arg Ser Leu Ser Val Lys Pro Arg Cys Phe Leu Met
 450 455 460
 Pro Glu Asn Asn Gly Ile Lys Ile Ser Val Trp Tyr Gln Thr Asn Ser
 465 470 475 480
 Tyr Ala Thr Met Ser Leu Arg Ser Lys Ile Val Ala Glu Ile Val Glu
 485 490 495
 Ala Phe Leu Lys Glu Glu Asn Ile His Ile Ala Tyr Thr Thr Ser Lys
 500 505 510
 Leu Leu Lys Val Asp Ala Asp Ala Leu Gly Asp Gly Phe Gly Asn Lys
 515 520 525
 Arg Glu Gln Lys
 530

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459

Arg Ser Glu Arg Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser
 1 5 10 15
 Tyr Lys Val Phe Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys
 20 25 30
 Ala Leu Ile Ile Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr
 35 40 45
 Leu Leu Glu Arg Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu
 50 55 60
 Ser Gly Glu Lys Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn
 65 70 75 80
 Asn Ala Phe Glu Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu
 85 90 95
 Gly Gly Gly Val Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr
 100 105 110
 Phe Arg Gly Ile Asp Phe Ile Asn Ile Pro Thr Thr Leu Ala Gln
 115 120 125
 Val Asp Ala Ser Val Gly Gly Lys Thr Gly Ile Asn Thr Pro Tyr Gly
 130 135 140
 Lys Asn Leu Ile Gly Ser Phe His Gln Pro Lys Ala Val Tyr Met Asp
 145 150 155 160
 Leu Ala Phe Leu Lys Thr Leu Glu Lys Arg Glu Phe Gln Ala Gly Val
 165 170 175
 Ala Glu Ile Ile Lys Met Ala Val Cys Phe Asp Lys Asn Leu Val Glu
 180 185 190
 Arg Leu Glu Thr Lys Asp Leu Lys Asp Cys Leu Glu Glu Val Ile Phe
 195 200 205
 Gln Ser Val Asn Ile Lys Ala Gln Val Val Val Gln Asp Glu Lys Glu
 210 215 220
 Arg Asn Ile Arg Ala Gly Leu Asn Tyr Gly His Thr Phe Gly Met Leu

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```

225          230          235          240
Ile Glu Asn Glu Thr Asn Tyr Glu Arg Phe Leu His Gly Glu Ala Ile
          245          250          255
Ala Ile Gly Met Arg Met Ala Asn Asp Leu Ala Leu Ser Leu Gly Met
          260          265          270
Leu Thr Leu Lys Glu Tyr Glu Arg Ile Glu Asn Leu Leu Lys Lys Phe
          275          280          285
Asp Leu Ile Phe Asn Tyr Gln Ile Thr Asp Ile Gln Lys Phe Tyr Glu
          290          295          300
Arg Leu Phe Leu Asp Lys Lys Ser Glu Asn Gln Thr Leu Lys Phe Ile
305          310          315          320
Leu Pro Lys Gly Val Gly Ala Phe Glu Ile Ala Ser His Ile Pro Lys
          325          330          335
Glu Thr Ile Leu Lys Val Leu Glu Lys Trp His
          340          345

```

(2) INFORMATION FOR SEQ ID NO:1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460

```

Lys Ser Lys Ser Met Lys Leu Arg Arg Gly Lys Ile Met Pro Phe Ser
1          5          10          15
Lys Phe Leu Glu Asn Leu Thr Ala Pro Phe Lys Arg Ile Lys Asn Arg
          20          25          30
Ser Leu Val Leu Ala Leu Gly Phe Leu Ile Leu Thr Phe Cys Leu Leu
          35          40          45
Leu Phe Leu Ile Leu Ser Asp Val Ser Arg Leu Ile Ser Ser Lys Asp
          50          55          60
Phe Leu Tyr Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp
65          70          75          80
Glu Asn Tyr Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu
          85          90          95
Ala Phe Leu Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys
          100          105          110
Arg Glu Ser Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe
          115          120          125
Phe Ile Ser Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg
          130          135          140
Leu Asp Thr Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu
145          150          155          160
Asn Ala Phe Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile
          165          170          175
Ala Gly Val Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr
          180          185          190
Leu Lys Lys Pro
          195

```

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(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461

```

Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp
1          5          10          15
Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu
20          25          30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
35          40          45
Leu Lys Lys Ile Leu Leu Glu Asn Arg Lys Lys Ser Val Leu Glu
50          55          60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
65          70          75          80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
85          90          95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
100         105         110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
115         120         125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
130         135         140
Leu Ile Asn Lys Tyr Leu Pro Ser Ala Gln Ser Gln Leu Pro Leu Lys
145         150         155         160
Ile Ser Lys Asp Ser Asp Gly Leu Leu Val Gln Phe Gly Val Ser Ile
165         170         175
Asp Leu Gln

```

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462

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```

Phe Lys Arg Tyr Phe Ile Thr Met Lys Ile Phe Gly Thr Asp Gly Val
1      5      10      15
Arg Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu
20      25      30
Gly Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys
35      40      45
Ile Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn
50      55      60
Ala Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile
65      70      75
Gly Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg
85      90      95
Cys Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp
100     105     110
Asn Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu
115     120     125
Glu Glu Arg Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His
130     135     140
Ser Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp
145     150     155
Asp Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys
165     170     175
His Leu Asn Leu Gln Lys Leu Arg Ile Val Leu Asp Thr Ala Asn Gly
180     185     190
Ala Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp
195     200     205
Val Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Glu Gln
210     215     220
Cys Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr
225     230     235
Arg Ala Asp Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val
245     250     255
Val Ala Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly
260     265     270
Val Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala
275     280     285
Val Val Ala Thr Ser Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys
290     295     300
Ser Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val
305     310     315
Ser Glu Cys Met Arg Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser
325     330     335
Gly His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val
340     345     350
Cys Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Leu Val Ser
355     360     365
Ser Ile Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn
370     375     380
Leu Asn Ile Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser
385     390     395
Ala Leu Leu Lys Glu Leu Asp Gln Leu Glu Ile Arg His Leu Ile Arg
405     410     415
Tyr Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp
420     425     430
Glu Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu
435     440     445
Gly Gln Leu Cys
450

```

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463

```

Asn His Gln Arg Ile Arg Ser Arg Gln Gln Phe Arg Lys Pro Phe Asp
1          5          10          15
Pro Phe Arg Arg Ala Ser Glu Leu Lys Val Arg Ser Cys Lys Gln Ile
20          25          30
Phe Asp Lys Lys Gly Leu Lys Pro Tyr Tyr Lys His Ser Val Cys Leu Lys
35          40          45
Pro Phe Phe Arg Phe Cys Phe Leu Lys Ile His Ala Tyr Gln Gln Arg
50          55          60
Tyr Arg Ala Phe Ala Leu Thr Leu Phe Ser Cys Lys Phe Phe Asn Ala
65          70          75          80
Cys Lys Ile Phe Ile Pro Ile Ile Asp Phe Lys Ile Val Phe Ile Pro
85          90          95
Ile Leu Lys His Gln Ala Lys Leu Lys Arg Val Ser Asn Ala Tyr
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464

```

Lys Arg Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala
1          5          10          15
Cys Ser Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys
20          25          30
Lys Ile Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn
35          40          45
Glu Asn Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu
50          55          60
Gly Tyr Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe
65          70          75          80
Ser Pro Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val
85          90          95
Val Tyr Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu

```

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      100      105      110
Ser Leu Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu
      115      120      125
Gln Leu Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr
      130      135      140
Ile Gln Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser
      145      150      155      160
Leu Ile Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn
      165      170      175
Cys Ile Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly
      180      185      190
Ile Ile Ile Leu Lys Ala Cys Ala
      195      200

```

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465

```

Lys Glu Ser Leu Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu
1      5      10      15
Phe Thr Ala Ser Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala
      20      25      30
Ser Ser Tyr Gln Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu
      35      40      45
Ile Leu Asp Gly Leu Asp Gly Arg Val Ala Arg Leu Thr Asn Thr Thr
      50      55      60
Ser Lys Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe
      65      70      75      80
Gly Val Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe
      85      90      95
Gly Arg Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala
      100      105      110
Ile Arg Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr
      115      120      125
Ser Phe Ile Gly Ile Pro Ile Pro Ala Ala Val Leu Val Val Leu
      130      135      140
Cys Val Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu
      145      150      155      160
Lys Leu Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser
      165      170      175
Asn Ile Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu
      180      185      190
Phe Ile Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu
      195      200      205
Glu Ala Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile
      210      215      220
Arg Trp Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser
      225      230      235      240

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Ala

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466

```

Tyr Leu Pro Ala Ser Glu Asn Ala Pro Leu Pro Ser Ser Val Phe Ser
1      5      10      15
Ser Ile Val Ala Leu Ser Leu Lys Ile Asp Ser Leu Phe Ser Leu Phe
20      25      30
Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro Phe Ala Leu Arg
35      40      45
Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His Tyr Gly Leu Glu
50      55      60
Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu Lys Val Gly Val
65      70      75      80
Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe Leu Leu Glu Arg
85      90      95
Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile Arg Ser Val Leu
100     105     110
Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln Lys Val Lys Ala
115     120     125
Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln Lys Lys Glu Leu
130     135     140
Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn Lys Asp Arg Asn
145     150     155     160
Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe Lys Glu Leu Gln
165     170     175
Glu His Ala Leu Phe Glu Ala Phe Asn Ala Ile Lys Thr Ser Thr Phe
180     185     190
Glu Ser Leu Asp Ser Lys Ile Glu Ala Tyr Phe Gly Leu His Ala Pro
195     200     205
Leu Glu Glu Tyr Phe Lys Ser Val Leu Val Met Asp Lys Asp Ile Glu
210     215     220
Ile Gln Lys Asn Arg Lys Asn Phe Leu Trp Gly Val Tyr Gln Ser Phe
225     230     235     240
Leu Glu Ile Gly Asp Ile Lys Glu Ile Ala Ile
245     250

```

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467

```

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1      5      10      15
Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
20      25      30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
35      40      45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
50      55      60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu
65      70      75      80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
85      90      95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
100     105     110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
115     120     125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
130     135     140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
145     150     155     160
His Val Lys Phe Ile Phe Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
165     170     175
Ile Leu Gly Gln Leu Gln Ile Phe Ser Lys Lys Ala Phe Gln Lys Asp
180     185     190
Tyr Phe Glu Lys Asn Pro Leu Leu Ile Pro Val Ser Ser Gly Pro Tyr
195     200     205
Val Ile Ala Ser Phe Asp Val Gly Lys Lys Ile Thr Tyr Gln Arg Asn
210     215     220
Pro Asn Tyr Trp Ala Lys Asn Leu Pro Ser Arg Lys Gly Gln Phe Asn
225     230     235     240
Phe Asp Gln Ile Lys Phe Glu Tyr Tyr Lys Asp Glu Thr Val Ala Leu
245     250     255
Gln Ala Phe Leu Ser Gly Ala Tyr Asp Trp Arg Leu Glu Ser Thr Ala
260     265     270
Lys Val Trp Ala Arg Gly Tyr Val Gly Lys Ala Met Asp Asn Lys Lys
275     280     285
Ile Thr Lys Tyr Leu Ile Ala His Lys Met Pro Ser Gly Met Gln Gly
290     295     300
Phe Phe Phe Asn Thr Arg Arg Glu Ile Phe Lys Asp Lys Arg Val Arg
305     310     315     320
Glu Ala Leu Phe Tyr Ala Phe Asp Phe Glu Trp Ala Asn Lys Asn Leu
325     330     335
Phe Phe Ser Gln Tyr Lys Arg Thr Thr Ser Phe Phe Ser Asn Ser Ile
340     345     350
Tyr Ala Ser Pro Pro Leu Pro Ser Pro Glu Glu Lys Ala Leu Leu Ala
355     360     365
Pro Tyr Glu Lys Ser Leu Asp Glu Arg Val Phe Lys Glu Pro Tyr Ile
370     375     380
Val Pro Arg Thr Asp Gly Pro Asp Val Leu Gly Tyr Asn Leu Arg Glu
385     390     395     400
Asn Leu Lys Tyr Ala Gln Lys Leu Leu Glu Ser Ala Gly Phe Ser Tyr
405     410     415

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Lys Asn Met Arg Leu Val Asp Lys Asn Asn Lys Pro Phe Ser Phe Thr
 420 425 430
 Leu Leu Leu Asn Ser Pro Ala Phe Glu Arg Leu Ala Leu Ala Phe Ala
 435 440 445
 Lys Asn Leu Arg Val Leu Gly Ile Glu Met Lys Ile Gln Arg Val Asp
 450 455 460
 Leu Ser Gln Tyr Val Asn Arg Ile Lys Ser Tyr Asp Phe Asp Met Ile
 465 470 475 480
 Val Gly Val Ile Gly Gln Ser Ser Phe Pro Gly Asn Glu Gln Arg Phe
 485 490 495
 Tyr Phe Gly Ser Leu Ser Ala Lys Ala Lys Gly Thr Arg Asn Tyr Ala
 500 505 510
 Arg Ile Ser Ser Lys Ala Val Asp Asp Leu Ile Glu Arg Ile Ile His
 515 520 525
 Ala Lys Asp Tyr Lys Glu Gln Leu Ala Ala Ile Gln Ala Met Asp Arg
 530 535 540
 Val Leu Leu Arg Gly Phe Tyr Ala Ile Pro His Phe Tyr Leu Pro Asn
 545 550 555 560
 Tyr Arg Ile Ala Ala Tyr Asn Tyr Ile Gly Met Pro Glu Ile Ser Pro
 565 570 575
 Ser Tyr Gly Phe Ser Pro Tyr Leu Trp Trp Ile Lys Lys Glu Arg Gly
 580 585 590
 Pro Lys

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468

Ser Val Ile Gly Val Tyr Ile Ile Ser Leu Lys Glu Ser Gln Arg Arg
 1 5 10 15
 Leu Asp Thr Glu Lys Leu Val Leu Glu Ser Asn Glu Lys Phe Lys Gly
 20 25 30
 Arg Cys Val Phe Gln Ile Phe Asp Ala Ile Ser Pro Lys His Gln Asp
 35 40 45
 Phe Glu Lys Leu Leu Gln Glu Leu Tyr Asn Ala Gln Ser Leu Leu Gln
 50 55 60
 Ser Asp Trp Tyr His Ser Tyr Val Gly Ala Gly Leu Thr Leu Pro Glu
 65 70 75 80
 Leu Gly Cys Tyr Leu Ser His Tyr Leu Leu Trp Lys Glu Cys Val Lys
 85 90 95
 Leu Asp Gln Pro Val Val Ile Leu Glu Asp Asp Val Thr Leu Glu Ser
 100 105 110
 His Phe Met Gln Ala Leu Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe
 115 120 125
 Val Arg Leu Tyr Gly Cys Tyr Trp Tyr Tyr His Glu Thr Lys Phe His
 130 135 140
 Val Leu Pro Lys Glu Phe Val Phe Pro Pro Phe Asp His Ser Phe Lys

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145          150          155          160
Asn Asn Pro Ile Leu Glu Lys Phe Lys Lys Phe Phe Asp Val Ser Arg
          165          170          175
Phe Leu Asn Leu Ser Thr His Lys Val Ile His Leu Tyr Ser Gln Lys
          180          185          190
Asn Thr Lys Lys Leu Leu Arg Asn Ala
          195          200

```

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469

```

Phe Ser Glu Arg Asp Phe Glu Leu Phe Arg Gln Lys Thr Asn Pro Tyr
1          5          10          15
Glu Arg Cys Ser Cys Gly Phe Gly Phe Leu Ser Asp Ala Ser Lys Arg
          20          25          30
Ser Leu Asn Pro Thr Leu Met Met Asn Asn Asn Asn Thr Leu Pro Lys
          35          40          45
Pro Leu Glu Glu Ser Leu Asp Leu Lys Glu Phe Ile Ala Leu Phe Lys
          50          55          60
Thr Phe Phe Ala Lys Glu Arg Gly Ser Ile Ala Leu Glu Asn Asp Leu
65          70          75          80
Lys Gln Ala Phe Thr Tyr Leu Asn Glu Val Asp Ala Ile Gly Leu Pro
          85          90          95
Ala Pro Lys Ser Val Lys Glu Ser Asp Leu Ile Val Val Lys Leu Thr
          100          105          110
Lys Leu Gly Thr Leu His Leu Asp Glu Ile Tyr Glu Ile Val Lys Arg
          115          120          125
Leu Arg Tyr Ile Val Val Leu Gln Asn Ala Phe Lys Pro Phe Thr His
130          135          140
Leu Lys Phe His Glu Arg Leu Asn Ala Ile Ile Leu Pro Pro Phe Phe
145          150          155          160
Asn Asp Leu Ile Leu Leu Asp Asp Glu Gly Gln Ile Lys Gln Gly
          165          170          175
Ala Asn Ala Thr Leu Asp Ala Leu Asn Glu Ser Leu Asn Arg Leu Lys
          180          185          190
Lys Glu Ser Thr Lys Ile Ile His His Tyr Ala His Ser Lys Glu Leu
          195          200          205
Ala Pro Tyr Leu Val Asp Thr Gln Ser His Leu Lys His Gly Tyr Glu
210          215          220
Cys Leu Leu Leu Lys Ser Gly Phe Ser Ser Ala Ile Lys Gly Val Val
225          230          235          240
Leu Glu Arg Ser Ala Asn Gly Tyr Phe Tyr Leu Leu Pro Glu Ser Ala
          245          250          255
Gln Lys Ile Ala Gln Lys Ile Ala Gln Ile Gly Asn Glu Ile Asp Cys
          260          265          270
Cys Ile Val Glu Met Cys Gln Thr Leu Ser Arg Ser Leu Gln Lys His
275          280          285

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Leu Leu Phe Leu Lys Phe Leu Phe Lys Glu Phe Asp Phe Leu Asp Ser
 290                295                300
Leu Gln Ala Arg Leu Asn Phe Ala Lys Ala Tyr Asn Leu Glu Phe Val
 305                310                315                320
Met Pro Ser Phe Thr Gln Lys Lys Met Ile Leu Glu Asn Phe Ser His
                325                330                335
Pro Ile Leu Lys Glu Pro Lys Pro Leu Asn Leu Lys Phe Glu Lys Ser
                340                345                350
Met Leu Ala Val Thr Gly Val Asn Ala Gly Gly Lys Thr Met Leu Leu
                355                360                365
Lys Ser Leu Leu Ser Ala Ala Phe Leu Ser Lys His Leu Ile Pro Met
                370                375                380
Lys Ile Asn Ala His His Ser Thr Ile Pro Tyr Phe Arg Glu Ile His
 385                390                395                400
Ala Ile Ile Asn Asp Pro Gln Asn Ser Ala Asn Asn Ile Ser Thr Phe
                405                410                415
Ala Gly Arg Met Lys Gln Phe Ser Ala Leu Leu Ser Lys Glu Asn Met
                420                425                430
Leu Leu Gly Val Asp Glu Ile Glu Leu Gly Thr Asp Ala Asp Glu Ala
                435                440                445
Ser Ser Leu Tyr Lys Thr Leu Leu Glu Lys Leu Leu Lys Gln Asn Asn
 450                455                460
Gln Ile Val Ile Thr Thr His His Lys Arg Leu Ser Val Leu Met Ala
 465                470                475                480
Glu Asn Lys Glu Val Glu Leu Leu Ala Ala Leu Tyr Asp Glu Glu Lys
                485                490                495
Glu Arg Pro Thr Tyr Thr Phe Leu Lys Lys Gly Val Ile Gly Lys Ser Tyr
                500                505                510
Ala Phe Glu Thr Ala Leu Arg Tyr Gly Val Pro Pro Phe Leu Ile Glu
                515                520                525
Lys Arg Lys Pro Ser Met Ala Lys Ile Arg Lys Asn
 530                535                540

```

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470

```

Lys Leu Thr Glu Lys Ile Met Leu Glu Thr Pro Lys Val Leu Leu Lys
 1                5                10                15
Asn Leu Gln Asp Cys Lys Ile His Phe Ile Gly Ile Gly Gly Ile Gly
                20                25                30
Ile Ser Gly Leu Ala Lys Tyr Leu Lys Ala Gln Gly Ala Lys Ile Ser
                35                40                45
Gly Ser Asp Ile Ala Ile Ser Pro Ser Val Lys Tyr Leu Lys Ala Leu
 50                55                60
Gly Val Glu Ile Asn Ile Pro His Asp Pro Lys Ala Ile Asn His Gln
 65                70                75                80
Asp Val Ile Ile His Ser Ala Ile Ile Lys Glu Asp Asn Thr Glu Ile

```

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```

      85                      90                      95
Gln Arg Ala Lys Glu Leu Glu Ile Pro Ile Leu Ser Arg Lys Asp Ala
      100                      105                      110
Leu Tyr Ser Ile Leu Lys Asp Lys Arg Val Phe Ser Val Cys Gly Ala
      115                      120                      125
His Gly Lys Ser Ser Ile Thr Ala Met Leu Ser Ala Ile Cys Pro Ala
      130                      135                      140
Phe Gly Ala Ile Ile Gly Ala His Ser Lys Glu Phe Asp Ser Asn Val
      145                      150                      155                      160
Arg Glu Ser Ala Asp Met Ser Leu Val Phe Glu Ala Asp Glu Ser Asp
      165                      170                      175
Ser Ser Phe Leu Phe Ser Asn Pro Phe Cys Ala Ile Val Pro Asn Thr
      180                      185                      190
Glu Pro Glu His Leu Glu His Tyr Asp His Asp Leu Glu Arg Phe Phe
      195                      200                      205
Phe Ala Tyr Lys Tyr Phe Leu Asp His Ala Gln Lys Arg Val Ile Tyr
      210                      215                      220
Lys Glu Asp Pro Phe Leu Lys Asn Tyr Ser Lys Asp Ala Ile Val Leu
      225                      230                      235                      240
Glu Lys Lys Asp Ile Tyr Asn Ile Gln Tyr Ile Leu Lys Asp Gly Glu
      245                      250                      255
Pro Tyr Thr Ser Phe Glu Leu Lys Asn Leu Gly Ala Phe Leu Val Trp
      260                      265                      270
Gly Leu Gly Glu His Asn Ala Thr Asn Ala Ser Leu Ala Ile Leu Ser
      275                      280                      285
Ala Leu Asp Glu Leu Asn Leu Glu Glu Ile Arg Asn Asn Leu Leu Asn
      290                      295                      300
Phe Lys Gly Ile Lys Lys Arg Phe Asp Ile Leu Gln Lys Asn Asp Leu
      305                      310                      315                      320
Ile Leu Ile Asp Asp Tyr Ala His His Pro Thr Glu Ile Gly Thr Thr
      325                      330                      335
Leu Lys Ser Ala Arg Ile Tyr Ala Asn Leu Leu Asn Thr Gln Glu Lys
      340                      345                      350
Ile Ile Val Ile Trp Gln Ala His Lys Tyr Ser Arg Leu Met Asp Asn
      355                      360                      365
Leu Glu Glu Phe Lys Lys Cys Phe Leu Glu His Cys Asp Arg Leu Ile
      370                      375                      380
Ile Leu Pro Val Tyr Ser Ala Ser Glu Val Lys Arg Asp Ile Asp Leu
      385                      390                      395                      400
Lys Ala His Phe Lys His Tyr Asn Pro Thr Phe Ile Asp Arg Val Arg
      405                      410                      415
Lys Lys Gly Asp Phe Leu Glu Leu Leu Val Asn Asp Asn Val Val Glu
      420                      425                      430
Thr Ile Glu Lys Gly Phe Val Ile Gly Phe Gly Ala Gly Asp Ile Thr
      435                      440                      445
Tyr Gln Leu Arg Gly Glu Met
      450                      455

```

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471

```

Ala Val Thr Ala Ile Leu Gly Trp Asp Glu Glu Gly Lys Leu Lys Phe
 1           5           10           15
Gly Lys Ile Arg His Lys Tyr Leu Glu Thr Ser Asn Val Asn Ala Gly
      20           25           30
Asn Ala Leu Thr Asn Leu Ile Leu Met Gln Arg Gly Tyr Ser Met Asn
      35           40           45
Ala Arg Ala Phe Gly Ala Gly Asp Asp Met Ile Lys Glu Ala Ile Ser
      50           55           60
Leu Lys Lys
65

```

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472

```

Lys Leu His Arg Gly Ser Gln Lys Gln Asn Pro Ile Asn Asp Pro Thr
 1           5           10           15
Trp Glu Ile Val Gly Phe Asp Ser Ala Thr His Lys Met Lys Ser Ala
      20           25           30
Pro Met Thr Leu Asp Phe Lys Gly Asn Lys Leu Thr Tyr Ser Leu Asp
      35           40           45
Lys Ser Glu Asn Met Ile Leu Thr Lys Leu Phe Tyr Gln Asp Ser Lys
      50           55           60
Leu Leu Lys Thr Ser Gln Glu Arg Lys Pro Arg Gly Ile Phe Arg Asp
      65           70           75           80
Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
      85           90           95
Val Val Glu Pro Val Ala Arg Ile Gly Ile Leu Ala Phe Thr Asn Asp
      100          105          110
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
      115          120          125
Thr Ile Asn Gly Glu Asn Arg Pro Leu Ser Gly Asn Arg His Phe Arg
      130          135          140
Val Gly Arg Arg Gly Gln Ala Gln Val Trp Glu Asn Gln Ala Gln Ile
      145          150          155          160
Phe Arg Asn Glu Gln Arg Glu Cys Arg Glu Arg Pro Asn Gln Ser His
      165          170          175
Phe Asn Ala Lys Arg Leu Phe Tyr Glu Arg
      180          185

```

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473

```

Trp Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser
1          5          10          15
Pro Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu
20          25          30
Arg Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu
35          40          45
Ala Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser
50          55          60
Lys Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His
65          70          75          80
Lys Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu
85          90          95
Leu Ile Ile Ser Asp Ala Asn Lys Glu Ala Tyr Thr Ile Thr Gln Lys
100         105         110
Tyr Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser
115         120         125
Lys Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val
130         135         140
Glu Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn
145         150         155         160
Ala Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu
165         170
  
```

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474

```

Met Gln Lys Ser Ile Phe Lys Ile Thr Leu Leu Leu Val Phe Leu Phe
1          5          10          15
Leu Arg Asn Ala Val Gly Leu Asp Asp Lys Lys Ala Ala Pro Lys Ser
20          25          30
  
```

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Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
 35 40 45
 Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
 50 55 60
 Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu
 65 70 75 80
 Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met
 85 90 95
 Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn
 100 105 110
 Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
 115 120 125
 Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu
 130 135 140
 His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro
 145 150 155 160
 Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
 165 170 175
 Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
 180 185 190
 Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
 195 200 205
 Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
 210 215 220
 Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys
 225 230 235 240
 Asn Lys Pro Ala Leu Val Glu Lys
 245

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475

Ser Gly Cys Tyr Phe Glu Ser Asn Ser Asp Val Tyr Val Val Ile Ile
 1 5 10 15
 Gly Leu Ala Asp Gln Lys Ile Gly Val Ile Val Asp Tyr Leu Ile Gly
 20 25 30
 Gln Glu Glu Val Val Ile Lys Ser Leu Gly Tyr Tyr Leu Lys Asn Thr
 35 40 45
 Arg Gly Ile Ala Gly Ala Thr Val Arg Gly Asp Gly Lys Ile Thr Leu
 50 55 60
 Ile Val Asp Val Gly Ala Met Met Glu Met Ala Lys Ser Ile Lys Val
 65 70 75 80
 Asn Ile Thr Thr Leu Met Asn Glu Ser Glu Asn Thr Lys Ser Lys Asn
 85 90 95
 Ser Pro Ser Asp Tyr Val Val Leu Ala Ile Asp Asp Ser Ser Thr Asp
 100 105 110
 Arg Ala Ile Ile Arg Lys Cys Leu Lys Pro Leu Gly Ile Thr Leu Leu

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```

      115      120      125
Glu Ala Thr Asn Gly Leu Glu Gly Leu Glu Met Leu Lys Asn Gly Asp
130      135      140
Lys Ile Pro Asp Ala Ile Leu Val Asp Ile Glu Met Pro Lys Met Asp
145      150      155      160
Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys Tyr Asn Lys Phe Lys Asn
165      170      175
Leu Pro Leu Ile Ala Val Thr Ser Arg Val Thr Lys Thr Asp Arg Met
180      185      190
Arg Gly Val Glu Ser Gly Met Thr Glu Tyr Ile Thr Lys Pro Tyr Ser
195      200      205
Gly Glu Tyr Leu Thr Thr Val Val Lys Arg Ser Ile Lys Leu Glu Gly
210      215      220
Asp Gln Ser
225

```

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476

```

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Glu Leu Ser Pro
1      5      10      15
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val
20      25      30
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His Leu Glu Leu
35      40      45
Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly Lys Arg Leu
50      55      60
Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp Phe Tyr Gly
65      70      75      80
Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg Pro Glu Thr
85      90      95
Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln Tyr His Leu
100      105      110
Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val Ser Val Ser
115      120      125
Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser Asp Ile Ser
130      135      140
Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg Phe Cys Leu
145      150      155      160
Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp His Met Pro
165      170      175
Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala Arg Asn Tyr
180      185      190
Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala Leu Phe Gly
195      200      205
Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe Leu Ala Ala
210      215      220

```

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Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr Asp Gln Leu
 225 230 235 240
 Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp Ala Glu Phe
 245 250 255
 Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly Val Leu Lys
 260 265 270
 Ser Phe Leu Arg
 275

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477

Lys Ala Val Leu Phe Asn Pro Leu Pro Thr Lys Arg Ser Val Met Pro
 1 5 10 15
 His Ser Leu Lys Lys Arg Phe Leu Ile Val Tyr Thr Leu Ser Thr Leu
 20 25 30
 Leu Leu Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn
 35 40 45
 Asn Leu Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala
 50 55 60
 Ile Ala Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro
 65 70 75 80
 Leu Lys Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu
 85 90 95
 Asp Ala Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala
 100 105 110
 Ser Phe Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys
 115 120 125
 Lys Gln Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly
 130 135 140
 Val Ser Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile
 145 150 155 160
 Pro Leu Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe
 165 170 175
 Val Ala Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
 180 185

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478

```

Asn Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu
1      5      10      15
Leu Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys
20      25      30
Phe Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys
35      40      45
Asp Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser
50      55      60
Ile Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe
65      70      75      80
Phe Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro
85      90      95
Glu Thr Leu Gly Tyr Leu Val Phe Ala Leu Leu Phe Leu Ala Ile Gln
100     105     110
Ser Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp
115     120     125
Lys Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp
130     135     140
Phe Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile
145     150     155     160
Tyr Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser
165     170     175
Ser Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Tyr
180     185     190
Pro Lys Ile Ala Gln Leu Phe Asn Gln Phe Thr Pro Leu Asn Asn Arg
195     200     205
Asp Leu Glu Ser Gln Ile Glu Ser Met Met Asp Lys Val Gly Phe Lys
210     215     220
Ser Gln Gly Ile Phe Val Met Asp Ala Ser Lys Arg Asp Gly Arg Leu
225     230     235     240
Asn Ala Tyr Phe Gly Gly Leu Gly Lys Asn Lys Arg Val Val Leu Phe
245     250     255
Asp Thr Leu Ile Ser Lys Val Gly Thr Glu Gly Leu Leu Ala Ile Leu
260     265     270
Gly His Glu Leu Gly His Phe Lys Asn Lys Asp Leu Leu Lys Asn Leu
275     280     285
Gly Ile Met Gly Gly Leu Leu Ala Leu Val Phe Ala Leu Ile Ala His
290     295     300
Leu Pro Pro Leu Val Phe Glu Gly Phe Asn Val Ser Gln Thr Pro Ala
305     310     315     320
Ser Leu Ile Thr Ile Leu Leu Leu Phe Leu Pro Val Phe Ser Phe Tyr
325     330     335
Ala Met Pro Leu Ile Gly Phe Phe Ser Arg Lys Asn Glu Tyr Asn Ala
340     345     350
Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys Glu Thr Leu Ala Lys Ala
355     360     365
Leu Val Ser Ile Val Asn Glu Asn Lys Ala Phe Pro Tyr Ser His Pro
370     375     380
Phe Tyr Val Phe Leu His Phe Thr His Pro Pro Leu Leu Glu Arg Leu
385     390     395     400
Lys Ala Leu Asp Tyr Glu Ile Glu
405

```

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(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479

```

Ile Arg Arg Arg Pro Ile Val Ser Asn Gln Leu Lys Asp Leu Phe Glu
1      5      10      15
Arg Gln Lys Glu Ala Asn Ala Ser Ser Lys Gln Glu Asp Asn Glu Glu
20      25      30
Ile Leu Gln Phe Ile Gly Phe Ile Ile Gly Asp Glu Glu Tyr Ala Ile
35      40      45
Pro Ile Leu Asn Ile Leu Glu Ile Val Lys Pro Ile Gly Tyr Thr Arg
50      55      60
Val Pro Glu Thr Pro Asn Tyr Val Leu Gly Val Phe Asn Leu Arg Gly
65      70      75      80
Asn Val Phe Pro Leu Ile Ser Leu Arg Leu Lys Phe Gly Leu Lys Ala
85      90      95
Glu Lys Gln Asn Lys Asp Thr Arg Tyr Leu Val Val Arg His Asn Asp
100     105     110
Arg Ser Leu Gly Phe Ser Ser Leu Ser Gly Leu Met Pro Ser Glu Ser
115     120     125
Ala Ser Thr Ile Asp Pro Ser Gln Lys Leu Cys Ala Ile Thr Ile Ile
130     135     140

```

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480

```

Ser Phe Ser Ile Asn Ser Phe Lys Lys Ala Lys Gly Met Lys Ser Thr
1      5      10      15
Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala Val Val Ile Val
20      25      30
Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys Val Glu Ser Val

```

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```

      35          40          45
Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys Ala Gln Leu Val
 50          55          60
Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe Met Gly Ala Asn
65          70          75          80
Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala Ile Asn Asp Thr
      85          90          95
Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala Asn Pro His Val
      100          105          110
Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Glu Arg Met Ile Thr
      115          120          125
Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn Thr Ala Leu Asn
      130          135          140
Glu Asn Met Thr Asn Gln Ile His Ser Leu Lys Ser Ile Thr Arg Ser
      145          150          155          160
Asp Pro Tyr Tyr Lys Glu Val Asn Gly Asp Lys Ile Tyr Gly Met Asp
      165          170          175
Ile Thr Leu Pro Leu Met Gly Lys Asn Gln Asn Val Ile Gly Ala Leu
      180          185          190
Asn Phe Phe Leu Asn Ile Asp Ala Phe Tyr Thr Asp Val Val Gly Lys
      195          200          205
Lys Lys Ser Asn Thr Phe Leu Met Gly Lys Asp Gly Arg Ile Leu Ile
      210          215          220
Asn Pro Asn Arg Glu Ile Gln Asp Lys Ile Leu Ser Ala Ile Asn Pro
      225          230          235          240
Asp Lys Arg Val Ala Lys Ala Val Glu Tyr Tyr Asn Gln Asn Glu Ala
      245          250          255
Gly Thr Leu Ser Tyr His Ser Leu Ser Gly Asn Thr Glu Thr Phe Leu
      260          265          270
Ala Ile Gln Pro Phe Asp Phe Phe Glu Glu Lys Gly Asn Asn Gly Gln
      275          280          285
Ser Leu Ala Leu Gly Asn Trp Glu Ile Cys Gln
      290          295

```

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481

```

Gly Val Phe Tyr Asn Ser Ser Leu Pro Gln Pro Pro Thr Lys Asn Pro
1          5          10          15
Leu Thr Arg Glu Tyr Arg Phe Leu Lys Arg Leu Ser Leu Ile Tyr Ala
      20          25          30
Ser Ser Phe Ile Val Phe Ile Leu Lys Asn Ala Leu Lys Leu Phe Leu
      35          40          45
Ile Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Leu Leu
      50          55          60
Val Lys Pro Phe Phe Tyr Leu Phe Asp Leu Val Ala His Leu Ser Thr
      65          70          75          80

```

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Arg Ile Asp Leu Ile Asp Lys His Val Lys Val Tyr His His Gln Lys
 85 90 95
 His His His Lys Pro
 100

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482

Phe Ile Thr Gly Ile Glu Ile His Pro Gly Ala Lys Ile Gly Arg Gly
 1 5 10 15
 Leu Phe Ile Asp His Gly Met Gly Val Val Ile Gly Glu Thr Thr Glu
 20 25 30
 Ile Gly Asp Asp Val Thr Ile Tyr His Gly Val Thr Leu Gly Gly Thr
 35 40 45
 Gly Lys Phe Lys Gly Lys Arg His Pro Thr Leu Gly Asn Arg Val Val
 50 55 60
 Val Gly Ala Gly Ala Lys Val Leu Gly Ala Ile Cys Val Gly Asp Asp
 65 70 75 80
 Val Arg Ile Gly Ala Asn Ala Val Val Leu Ser Asp Leu Pro Thr Gly
 85 90 95
 Ser Thr Ala Val Gly Ala Lys Ala Lys Thr Ile Thr Lys Asp Arg
 100 105 110

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483

Lys Gly Phe Leu Gly Val Lys Lys Val Ile Val Phe Ile Lys Lys Lys
 1 5 10 15
 Gly Glu Met Val Val Asn Ser Lys Val Gln Thr Leu Lys Val Phe Ser

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```

      20      25      30
Lys Phe Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu
      35      40      45
Glu Ala His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr
      50      55      60
Glu Ile Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu
      65      70      75      80
Thr Val Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe
      85      90      95
Lys Tyr Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala
      100      105      110
Leu Ala Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr
      115      120      125
Tyr Asn Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys
      130      135      140
Ser Leu Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe
      145      150      155      160
Asn Glu Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys
      165      170      175
His Pro Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys
      180      185      190
Ile Ala Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp
      195      200      205
Ile Ile Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp
      210      215      220
Asn Thr Leu Leu Thr Ser Glu Asn Arg Arg Ser Trp Arg Lys Lys Ile
      225      230      235      240
Gly Tyr Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp
      245      250      255
Asn Ile Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val
      260      265      270
Cys Lys Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu
      275      280      285
Lys Thr Gln Val Gly Glu Gly Gly Ala Lys Leu Ser Gly Gly Gln Lys
      290      295      300
Gln Arg Ile Gly Ile Ala Arg Ala Leu Tyr Asp Asn Pro Glu Ile Leu
      305      310      315      320
Val Leu Asp Glu Ala Thr Ser Ala Leu Asp Asn Glu Thr Glu Ser Lys
      325      330      335
Ile Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val
      340      345      350
Ile Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp
      355      360      365
Met Ser Gln His Lys Asp Asn Leu Gly
      370      375

```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...229

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484

```

Ala Tyr Lys Lys Gly Glu Ile Met Ala Leu Glu Val Val Leu Trp Asp
1      5      10      15
Phe Asp Gly Val Ile Phe Asp Ser Met His Leu Lys Tyr Glu Gly Phe
20     25     30
Lys Ala Leu Phe Gln Lys His Gly Asn Asp Ser Lys Glu Gly Leu Lys
35     40     45
Gln Phe Glu Val Tyr His Tyr Gln Ser Gly Gly Ile Ser Arg Asn Glu
50     55     60
Lys Ile Gln Tyr Phe Tyr Asn Glu Ile Leu Lys Thr Pro Ile Ala Gln
65     70     75     80
Glu Glu Ile Asp Ala Leu Ala Leu Glu Phe Gly Ala Ile Ile Glu Gln
85     90     95
Lys Leu Phe Asp Arg Gly His Leu Asn Ser Glu Val Met Ala Phe Ile
100    105    110
Asp Lys His Tyr Gln Asn Tyr Ile Phe His Ile Ala Ser Ala Ala Leu
115    120    125
His Ser Glu Leu Gln Val Leu Cys Glu Phe Leu Gly Ile Thr Lys Tyr
130    135    140
Phe Lys Ser Val Glu Gly Ser Pro Pro Asp Lys Pro Lys Ile Ile Ala
145    150    155    160
Asn Ile Ile Gln Lys Tyr Ala Tyr Asp Pro Ser Arg Met Leu Met Ile
165    170    175
Gly Asp Ser Val Asn Asp Tyr Glu Ser Ala Lys Ala Asn Lys Val Ala
180    185    190
Phe Leu Gly Tyr Asn Ser Lys Val Leu Lys Asn Leu Val Gly Gln Asp
195    200    205
Gly Tyr Gln Gly Lys Tyr Leu Glu Ser Phe Lys Gly Phe Asp Leu Gln
210    215    220
Asn Phe Ala Lys Glu
225

```

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485

```

Asn Lys Ser Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly
1      5      10      15
Lys Ser Ser Leu Ala Gln Glu Leu Gly Leu Ala Leu Lys Leu Glu Val
20     25     30
Leu Asp Thr Asp Met Ile Ile Ser Glu Arg Val Gly Leu Ser Val Arg
35     40     45
Gly Ile Phe Glu Glu Leu Gly Glu Asp Asn Phe Arg Met Phe Glu Lys
50     55     60
Asn Leu Ile Asp Glu Leu Lys Thr Leu Lys Thr Pro His Ile Ile Ser
65     70     75     80
Thr Gly Gly Gly Ile Val Met His Glu Asn Leu Lys Gly Leu Gly Thr

```

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```

      85              90              95
Thr Phe Tyr Leu Lys Met Asp Phe Glu Thr Leu Ile Lys Arg Leu Asn
      100              105              110
Gln Lys Glu Arg Glu Lys Arg Pro Leu Leu Asn Asn Leu Thr Gln Ala
      115              120              125
Lys Glu Leu Phe Glu Lys Arg Gln Ala Leu Tyr Glu Lys Asn Ala Ser
      130              135              140
Phe Ile Ile Asp Ala Arg Gly Gly Leu Asn Asn Ser Leu Lys Gln Val
      145              150              155              160
Leu Gln Phe Ile Ala
      165

```

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486

```

Ile Phe Phe Lys Gly Leu Val Met Leu Ser Arg Asp Ile Val Gln Tyr
1      5      10      15
Ser Lys Ile Arg Thr Glu Leu Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser
      20      25      30
His Asn Ile Arg Asn His Leu Pro Glu Ile Thr Leu Asp Tyr Leu Asn
      35      40      45
Arg Gln Ile Ser Lys Met Gln Ala Glu Ile Lys Met Ala Lys Ser Phe
      50      55      60
Phe Val Leu Asp Ala Lys Gly Met Leu Met Leu Lys Pro Ser Gln Phe
      65      70      75      80
Lys Glu Gln Gly His Lys Glu Gly Leu Leu Glu His Asp Leu Thr Glu
      85      90      95
Gly Ile Glu Leu Glu Ser His Val Ser Phe Ser Asp Lys Tyr Tyr Phe
      100      105      110
Tyr Gln Ala Val Asn Glu Lys Arg Cys Ile Leu Thr Asp Pro Tyr Pro
      115      120      125
Ser Lys Lys Gly Asn His Leu Val Val Ser Ala Ser Tyr Pro Val Tyr
      130      135      140
Asp Gln Asn Asn Asp Leu Ala Phe Val Val Cys Leu Gln Ile Pro Leu
      145      150      155      160
Arg Val Ala Ile Glu Ile Ser Ser Pro Ser Lys Tyr Phe Lys Thr Phe
      165      170      175
Ser Glu Gly Ser Met Val Met Tyr Phe Met Ile Ser Ile Met Leu Thr
      180      185      190
Leu Val Ser Leu Leu Leu Phe Val Lys Cys Ile Ser Ser Phe Trp Thr
      195      200      205
Ala Ile Val His Phe Ser Ser Phe Asp Ile Lys Glu Val Phe His Pro
      210      215      220
Ile Val Leu Leu Thr Leu Ala Leu Ala Thr Phe Asp Leu Val Lys Ala
      225      230      235      240
Ile Phe Glu Glu Glu Val Leu Gly Lys Asn Ser Gly Asp Asn His His
      245      250      255

```

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```

Ala Ile His Arg Thr Met Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala
      260      265      270
Leu Ala Ile Glu Ala Leu Met Leu Val Phe Lys Phe Ser Val Ser Glu
      275      280      285
Pro Asp Lys Ile Thr Tyr Ala Val Tyr Leu Ala Ile Gly Val Ala Val
      290      295      300
Leu Leu Ile Ser Leu Ala Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu
      305      310      315      320
Pro Lys Arg Glu Arg
      325

```

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487

```

Glu Ser Tyr Gln Thr Val Phe Thr Arg Gln Arg Tyr Tyr Gln Arg Leu
1      5      10      15
Phe Arg Arg Ala Val Cys Arg Asn Leu Arg Val Cys Glu Phe Thr Asn
      20      25      30
Gln Asn Asn Lys Arg Gly Asp Cys Gln Arg Gln Gln Leu Phe Tyr Gly
      35      40      45
Ala Tyr His Gly Glu Cys Leu Ser His Phe Arg Ile Ala Lys Thr His
      50      55      60
Cys Gly Ala Ser Pro Phe Ile Val Ser Asp Phe Asn Phe Ile Gly Phe
      65      70      75      80
Ile Val Pro Pro Ser Asn His Phe Ile Cys Gly Ser Gln Leu Lys Ser
      85      90      95
Arg Pro Phe Arg Ala Ile Cys Leu Ala Arg Ile Ser Lys His Cys Gln
      100      105      110
Ser Leu Phe Thr Leu Val Cys His Arg Val Phe Tyr Gly Val Pro Tyr
      115      120      125
Phe Met Leu Gly Val Ile Glu Arg Tyr Tyr Phe Trp His Asp His Glu
      130      135      140
Asn Pro Pro Ser Ile Gln Pro Ala Arg Tyr Arg Val Ser Gly Asn Cys
      145      150      155      160
Asp Arg Val Cys Gly His Tyr Phe Asn Arg Phe Gly Tyr His Gly Ala
      165      170      175
Phe Arg Arg Asn Gln Pro Gly Leu Arg Tyr Asn Leu
      180      185

```

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488

```

Gly Val Leu Arg Phe Ser Ile Phe Phe Lys Val Val Ala Leu Phe Met
1      5      10      15
Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser Ser
      20      25      30
Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln Phe
      35      40      45
Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg Ala
      50      55      60
Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile Glu
      65      70      75      80
Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His Arg
      85      90      95
Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe Ile
      100      105      110
Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His Ser
      115      120      125
Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu Leu
      130      135      140
Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu Arg
      145      150      155      160
Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser Val
      165      170      175
Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn Glu
      180      185      190
Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg Val
      195      200      205
Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr Lys
      210      215      220
Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys Arg
      225      230      235      240
Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe Ala
      245      250      255
Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu Lys
      260      265      270
Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu Ile
      275      280      285
Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr Ile
      290      295      300
Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met Ile
      305      310      315      320
Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp Phe
      325      330      335
Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys Glu
      340      345      350
Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro Ser
      355      360      365
Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala Leu
      370      375      380
Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg Ile
      385      390      395      400
Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu Glu
      405      410      415

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Ala Asp Asn Glu Glu Leu Pro Pro Pro Arg Lys Phe Glu Arg Gly Glu
 420 425 430
 Gly Asn Glu Gly Asn Arg Lys Ser Gln Leu Trp Gly
 435 440

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489

Arg Lys Thr Lys Arg Glu Asn Met Phe Lys Arg Leu Arg Arg Leu Arg
 1 5 10 15
 Ser Ser Glu Asn Leu Arg Ala Met Val Arg Glu Thr Arg Leu Asn Ile
 20 25 30
 Asn Asp Phe Ile Ala Pro Leu Phe Val Ile Glu Ser Asp Ser Gly Ile
 35 40 45
 Lys Asn Glu Ile Ser Ser Met Pro Gly Val Tyr Gln Met Ser Ile Glu
 50 55 60
 Pro Leu Leu Lys Glu Cys Glu Glu Leu Val Gly Leu Gly Ile Lys Ala
 65 70 75 80
 Val Leu Leu Phe Gly Ile Pro Lys His Lys Asp Ala Thr Gly Ser His
 85 90 95
 Ala Leu Asn Lys Asp His Ile Val Ala Lys Ala Thr Arg Glu Ile Lys
 100 105 110
 Lys Arg Phe Lys Asp Leu Ile Val Ile Ala Asp Leu Cys Phe Cys Glu
 115 120 125
 Tyr Thr Asp His Gly His Cys Gly Ile Leu Glu Asn Ala Ser Val Ser
 130 135 140
 Asn Asp Lys Thr Leu Lys Ile Leu Asn Leu Gln Gly Leu Ile Leu Ala
 145 150 155 160
 Glu Ser Gly Val Asp Ile Leu Ala Pro Ser Asn Met Met Asp Gly Asn
 165 170 175
 Val Leu Ser Leu Arg Lys Ala Leu Asp Lys Ala Gly Tyr Phe His Thr
 180 185 190
 Pro Ile Met Ser Tyr Ser Thr Lys Phe Ala Ser Ser Tyr Tyr Gly Pro
 195 200 205
 Phe Arg Asp Val Ala Asn Ser Pro Pro Ser Phe Gly Asp Arg Lys Ser
 210 215 220
 Tyr Gln Met Asp Tyr Ala Asn Gln Lys Glu Ala Leu Leu Glu Ser Leu
 225 230 235 240
 Glu Asp Glu Lys Gln Gly Ala Asp Ile Leu Met Val Lys Pro Ala Leu
 245 250 255
 Ala Tyr Leu Asp Ile Val Lys Glu Ile Arg Asp His Thr Leu Leu Pro
 260 265 270
 Leu Ala Leu Tyr Asn Val Ser Gly Glu Tyr Ala Met Leu Lys Leu Ala
 275 280 285
 Gln Lys His Asn Leu Ile Asn Tyr Glu Ser Val Leu Leu Glu Thr Met
 290 295 300
 Thr Cys Phe Lys Arg Ala Gly Ala Asp Met Ile Ile Ser Tyr His Ala

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305 310 315 320
Lys Glu Val Ala Asn Leu Leu Gln Arg Asn
 325 330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Gly | Arg | Ile | Leu | Ala | Glu | Asp | Ile | Ile | Cys | Val | His | Ala | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Lys | Phe | Asn | Gln | Ser | Ala | Met | Asp | Gly | Tyr | Gly | Phe | Lys | Met | Gln |
| | | | 20 | | | | | 25 | | | | 30 | | | |
| Asp | Leu | Gly | Gln | Lys | Thr | Gln | Val | Ile | Gln | His | Ile | Phe | Ala | Gly | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Val | Ser | Ala | Leu | Glu | Val | Lys | Glu | Asn | Glu | Cys | Val | Lys | Ile | Met |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Gly | Ala | Met | Val | Pro | Lys | Gly | Ile | Glu | Thr | Ile | Val | Pro | Ile | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Met | Leu | Glu | Ser | His | Lys | Asp | Phe | Ala | Leu | Ala | Pro | Lys | Asp | Phe |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Lys | Ile | His | Ala | Asn | Ile | Arg | Gln | Lys | Gly | Glu | Asn | Ala | Ser | Leu | Asn |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Ser | Val | Leu | Val | Pro | Lys | Asn | Thr | Arg | Leu | Asn | Tyr | Gly | His | Ile | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Ile | Ala | Ser | Gln | Gly | Phe | Lys | Glu | Ile | Lys | Ala | Phe | Arg | Lys | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Ile | Ala | Leu | Phe | Ser | Ser | Gly | Asp | Glu | Leu | Val | Pro | Leu | Gly | Gln |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asn | Ala | Leu | Glu | Cys | Gln | Val | Tyr | Asp | Val | Asn | Ser | Val | Gly | Val | Phe |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Asn | Met | Leu | Lys | Asn | Tyr | Asn | Thr | His | Phe | Leu | Gly | Val | Leu | Lys | Asp |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asp | Lys | Asn | Leu | Gln | Leu | Lys | Ile | Leu | Glu | Leu | Gln | Gly | Tyr | Asp | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ile | Leu | Ser | Ser | Ala | Gly | Val | Ser | Val | Gly | Asp | Lys | Asp | Phe | Phe | Lys |
| | 210 | | | | | 215 | | | | | | 220 | | | |
| Asp | Ala | Leu | Lys | Glu | Arg | Asn | Ala | Leu | Phe | Tyr | Tyr | Glu | Lys | Val | Asn |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Lys | Pro | Gly | Lys | Pro | Val | Thr | Leu | Ala | Gln | Leu | Asn | Gln | Ser | Ile |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Ile | Gly | Leu | Pro | Gly | Asn | Pro | Leu | Ser | Cys | Leu | Leu | Val | Leu | Arg |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Val | Leu | Ile | Leu | Pro | Leu | Leu | Glu | Arg | Leu | Ser | Leu | Asn | Lys | Asp | Phe |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Lys | Leu | Lys | Pro | Phe | Lys | Ala | Gln | Ile | Asn | Ala | Pro | Leu | Lys | Leu | Asn |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asn | Lys | Arg | Thr | His | Leu | Ile | Leu | Gly | Asn | Tyr | Ser | Asn | His | Gln | Phe |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Tyr | Asn | Asn | Arg | Tyr | Glu | Ser | Gly | Ala | Ile | Gln | Ala | Leu | Ala |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Gln | Val | Asp | Ser | Ile | Ala | Leu | Ile | Asp | Glu | Gly | Val | Gly | Leu | Val | Gln |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Gly | Glu | Ile | Glu | Ile | Leu | Arg | Phe | Glu | Asn | | | | | | |
| | | 355 | | | | | 360 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491

[illegible]

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492

```

Lys Ala Val Ala Thr Pro His His Thr Pro Leu Trp Leu Ser Val Tyr
1      5      10      15
Glu Ser Phe Lys Glu Ala Leu Asp Phe Lys Glu Val Ile Leu Val Val
20      25      30
Ser Glu Leu Asp Tyr Val Tyr Ile Gln Arg His Tyr Pro Lys Ile Lys
35      40      45
Leu Val Lys Gly Gly Ala Ser Arg Gln Glu Ser Val Arg Asn Ala Leu
50      55      60
Lys Val Ile Asp Ser Thr Tyr Thr Ile Thr Ser Asp Val Ala Arg Gly
65      70      75      80
Leu Ala Asn Met Glu Ala Leu Lys Ser Leu Phe Leu Thr Leu Gln Gln
85      90      95
Thr Ser His Tyr Cys Ile Ala Pro Tyr Leu Pro Cys Tyr Asp Thr Ala
100      105      110
Ile Tyr Tyr Asn Glu Ala Leu Asp Arg Glu Ala Ile Lys Leu Ile Gln
115      120      125
Thr Pro Gln Leu Ser His Thr Lys Thr Leu Gln Ser Ala Leu Asn Gln
130      135      140
Gly Gly Phe Lys Asp Glu Ser Ser Ala Ile Leu Gln Ala Phe Pro Asn
145      150      155      160
Ser Val Ser Tyr Ile Glu Gly Ser Lys Asp Leu His Lys Leu Thr Thr
165      170      175
Ser Gly Asp Leu Lys Phe Phe Thr Pro Phe Phe Asn Pro Ala Lys Asp
180      185      190
Thr Phe Ile Gly Met Gly Phe Asp Thr His Ala Phe Ile Lys Asp Lys
195      200      205
Pro Met Val Leu Gly Gly Val Val Leu Asp Cys Glu Phe Gly Leu Lys
210      215      220
Ala His Ser Asp Gly Asp Ala Leu Leu His Ala Val Ile Asp Ala Ile
225      230      235      240
Leu Gly Ala Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn
245      250      255
Asp Pro Lys Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val
260      265      270
Leu Asp Phe Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala
275      280      285
Thr Ile Phe Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile
290      295      300
Leu Glu Asn Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser
305      310      315      320
Leu Lys Val Thr Thr Met Glu Lys Met Gly Phe Ile Gly Lys Gln Glu
325      330      335
Gly Leu Leu Val Gln Ala His Val Ser Met Arg Tyr Lys Gln Lys Leu
340      345      350

```

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493

```

Cys Leu Gly Met Cys Phe Ile Leu Lys Pro Phe Leu Ser Cys Leu Lys
1      5      10      15
Trp Ala Asn Pro Ser Leu Lys Pro Leu Ser Asn Ala Val Leu Arg Leu
      20      25      30
Ser Arg Gly Glu Ile Glu Asp Val Phe Val Gly Glu Cys Phe Asn Ser
      35      40      45
Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu Asp Lys Thr Ala His Phe
      50      55      60
Ile Glu Ala Ser Leu Lys Ser Met Ala Ile Leu Asn Lys Asp Ala
      65      70      75      80
Lys Met Tyr Ala Asp Phe Gly Leu His Phe Gly Met Ala Phe Gln Ile
      85      90      95
Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp Ala Asn Thr Leu Gly Lys
      100      105      110
Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys Thr Thr Leu Pro Tyr Leu
      115      120      125
Leu Leu Tyr Glu Lys Leu Asn Gln His Glu Gln Gly Leu Leu Ile Ser
      130      135      140
Tyr Phe Lys Gln Asp Ser His Glu Ile Ile Glu Trp Thr Lys Glu Lys
      145      150      155      160
Phe Lys Gln His Gly Ile Ile Glu Glu Thr Leu Lys Ile Ala Gln Val
      165      170      175
Tyr Ser Lys Lys Ala Leu Glu Ala Ile Lys Gly Glu Asn Asn Leu Ile
      180      185      190
Leu Glu Lys Leu Ala Gln Asp Val Ile Tyr Arg Thr Phe
      195      200      205

```

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494

```

Lys Lys Val Lys Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly
1      5      10      15
Leu Phe Phe Leu Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn

```

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```

      20      25      30
Ser Phe Leu Gly Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser
      35      40      45
Lys Ala Ala Ser Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu
      50      55      60
Gly Cys Thr Gln Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg
      65      70      75      80
Ile Asp Tyr Lys Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala
      85      90      95
Asp Asp Arg Glu Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly
      100      105      110
Leu Gly Thr Ala Gln Asn Tyr Gln Glu Ala Ile Asp Ala Tyr Ala Arg
      115      120      125
His Ala Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495

```

Ser Ser Lys Thr Ala Phe Arg Ala Lys Gln Ile Ile Thr Ala Thr Asp
1      5      10      15
Ile Ser Ala Gln Lys Arg Gln Glu Arg Leu Ala Ser Met Gly Lys Ile
      20      25      30
Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val Gly Ser Ile Ser
      35      40      45
Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu Lys Thr Lys Pro
      50      55      60
Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val Glu Arg Ile Ile
      65      70      75      80
Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala Asn Arg Thr Lys
      85      90      95
Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu Ala Leu Asn Cys
      100      105      110
Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn Phe Ser Asp Glu
      115      120      125
Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val Leu Gln Asn Phe
      130      135      140
Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu Glu Ser Glu Gln
      145      150      155      160
Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu Phe Ile Val Phe
      165      170      175
Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys Ser Ala Leu Phe
      180      185      190
Glu Pro Phe Glu Thr Thr Lys Leu Lys Gly Asn Gly Leu Gly Leu Ala
      195      200      205
Leu Ser Leu Gln Val Val Lys Ala His Glu Gly Ser Ile Ala Leu Leu
      210      215      220

```

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Glu Asn Gln Glu Lys Thr Phe Glu Ile Lys Ile Leu Asn Ala Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496

Lys Pro Lys Thr Ile Leu Lys Lys Gly Leu Leu Met Lys Thr Phe Glu
 1 5 10 15
 Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val Leu Phe Met Lys Val
 20 25 30
 His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val His
 35 40 45
 Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp Asp
 50 55 60
 Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr Leu
 65 70 75 80
 Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr Ser
 85 90 95
 Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys His
 100 105 110
 Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly
 115 120 125
 Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln
 130 135 140
 Lys Ser Ile Trp Met Leu Glu Ala His Leu Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497

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Gly Ile Cys Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile
 1 5 10 15
 Ala Ser Trp Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe
 20 25 30
 Ser Lys Ile Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala
 35 40 45
 Leu Leu Asp Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn
 50 55 60
 Leu Cys Ala Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp
 65 70 75 80
 Asp Val Ile Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn
 85 90 95
 Ala Leu Phe Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr
 100 105 110
 Ser Lys Ala Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln
 115 120 125
 Ala Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498

Cys Met Leu Phe Ser Lys Leu Phe Ala Pro Thr Leu Lys Glu Pro Pro
 1 5 10 15
 Lys Asp Ala Val Leu Lys Ser Pro Lys His Pro Gly Asn Gly Gly His
 20 25 30
 Pro Leu Gln Ile Gly Ser Gly Ile Tyr Asn Phe Leu Pro Leu Ala Lys
 35 40 45
 Lys Val Leu Asp Lys Ile Glu Asn Val Thr His Lys Arg Met Gln Glu
 50 55 60
 His Gly Ala Gln Asn Ile Leu Met Ser Phe Val Val Leu Ala Ser Leu
 65 70 75 80
 Trp Glu Lys Ser Gly Arg Leu Asp Lys Tyr Gly Lys Glu Leu Leu Val
 85 90 95
 Phe Lys Asp Arg Lys Asp Asn Asp Phe Val Leu Ser Pro Thr Leu Glu
 100 105 110
 Glu Asn Ile Thr Glu Ile Ala Ala Asn Phe Ile Lys Ser Tyr Lys Gln
 115 120 125
 Leu Pro Val His Leu Tyr Gln Ile His Thr Lys Phe Arg Asp Glu Ile
 130 135 140
 Arg Pro Arg Phe Gly Leu Val Arg Ala Arg Glu Phe Ile Met Lys Asp
 145 150 155 160
 Gly Tyr Ser Phe His Glu Asp Ala Glu Ser Leu Asp Lys Glu Ile Leu
 165 170 175
 Asn Thr Gln Ser Ala Tyr Lys Glu Ile Leu Ser Asp Leu Gly Leu Asp
 180 185 190

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Phe Arg Ile Val Glu Ala Asp Ser Gly Ala Ile Gly Gly Ser Lys Ser
 195 200 205
 Arg Glu Phe Val Val Leu Thr Glu Cys Gly Glu Asp Thr Ile Val Val
 210 215 220
 Cys Gln Asn Cys Asp Tyr Ala Ala Asn Ile Glu Ile Ala Lys Arg Ser
 225 230 235 240
 Lys Arg Thr Glu Pro Leu Met Ser Pro Ser Ala Leu Ala Lys Phe Pro
 245 250 255
 Thr Pro Asn Thr Thr Ser Ala Pro Ser Val Ala Glu Phe Phe Lys Thr
 260 265 270
 Glu Pro Tyr Phe Val Leu Lys Ala Leu Val Asn Lys Val Ile His Lys
 275 280 285
 Asp Lys Glu Thr Leu Ala Cys Phe Phe Val Arg Gly Asp Asp Asn Leu
 290 295 300
 Glu Glu Thr Lys Ala Leu Asn Thr Leu Asn Leu Leu Gly Ala Asn Ala
 305 310 315 320
 Leu Glu Leu Arg Glu Ala Asn Glu Glu Asp Leu Asn Lys Ala Gly Leu
 325 330 335
 Ile Ala Gly Phe Ile Gly Pro Tyr Gly Leu Lys Lys His Val Cys Tyr
 340 345 350
 Ile Ile Phe Asp Glu Asp Leu Lys Glu Gly Asp Cys Leu Ile Val Gly
 355 360 365
 Ala Asn Glu Lys Asp Phe His Ala Val Gly Val Asp Leu Lys Gly Phe
 370 375 380
 Glu Asn Leu Val Tyr Ala Asp Ile Val Gln Val Lys Glu Ser Asp Cys
 385 390 395 400
 Cys Pro Asn Cys Gln Gly Ala Leu Lys Tyr His Lys Ser Leu Glu Val
 405 410 415
 Gly His Ile Phe Lys Leu Gly Gln Ser Tyr Ala Lys Ser Leu Lys Ala
 420 425 430
 Ser Phe Leu Asp Lys Asn Gly Lys Glu Arg Phe Phe Glu Met Gly Cys
 435 440 445
 Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu Glu Gln Lys
 450 455 460
 Ser Asp Asp Leu Gly Cys Val Trp Thr Lys Asn Thr Ala Pro Phe Asp
 465 470 475 480
 Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln Lys Lys Leu
 485 490 495
 Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val Asp Ala Leu
 500 505 510
 Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg Asp Phe Glu
 515 520 525
 Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln Thr Leu Glu
 530 535 540
 Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu Lys Gln Thr
 545 550 555 560
 Ile Lys Asp Ile Glu Leu Glu Glu Lys Ile Leu Glu Met Leu Ala Ser
 565 570 575
 Glu

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499

```

Ile Arg Glu Pro Gln Val Ala Ile Met Thr Ala Met Met Arg Tyr Phe
1          5          10          15
His Ile Tyr Ala Thr Thr Phe Phe Phe Pro Leu Ala Leu Leu Phe Ala
20          25          30
Val Ser Gly Leu Ser Leu Leu Phe Lys Ala Arg Gln Asp Thr Gly Ala
35          40          45
Lys Ile Lys Glu Trp Val Leu Glu Lys Ser Leu Lys Lys Glu Glu Arg
50          55          60
Leu Asp Phe Leu Lys Gly Phe Ile Lys Glu Asn His Ile Ala Met Pro
65          70          75          80
Lys Lys Ile Glu Pro Arg Glu Tyr Arg Gly Ala Leu Val Ile Gly Thr
85          90          95
Pro Leu Tyr Glu Ile Asn Leu Glu Thr Lys Gly Thr Gln Thr Lys Ile
100          105          110
Lys Thr Ile Glu Arg Gly Phe Leu Gly Ala Leu Ile Met Leu His Lys
115          120          125
Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly Ile Phe Cys Val
130          135          140
Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met Val Ala Phe Lys
145          150          155          160
Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly Ser Val Val Phe
165          170          175
Phe Gly Ala Ile Tyr Trp Ser Leu
180

```

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500

```

Leu Ile Lys Ser Lys Ser Lys Lys Trp Leu Leu Val Gly Glu Gly Ala
1          5          10          15
Asn Ser Glu Ile Phe Glu Ala Ser Met Gln Ser Leu Leu Lys Thr Asp
20          25          30
Gly Val Tyr Ser Asn His Lys Pro Ile Tyr Gln Glu Phe Tyr Glu Leu
35          40          45
Asn Ser His Asn Gly Leu Tyr Tyr Gln Pro Asn Val Phe Phe Ala Tyr
50          55          60
Glu Ser Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp Asn
65          70          75          80
Phe Ser Lys Phe Val Ser His Arg Leu Gln
85          90

```

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(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501

```

Met Leu Glu Ser Val Asn Val Lys Ile Ser Ala Asp Asp Ile Lys Ser
1      5      10      15
Lys Asn Val Ala Ala Val Met Ile Thr Ala Ser Leu Pro Pro Phe Ala
      20      25      30
Arg Gln Gly Asp Lys Ile Asp Ile His Ile Ser Ser Ile Gly Asp Ala
      35      40      45
Lys Ser Ile Gln Gly Gly Thr Leu Val Met Thr Pro Leu Asn Ala Val
      50      55      60
Asp Gly Asn Ile Tyr Ala Leu Ala Gln Gly Ala Ile Ile Ser Gly Asn
      65      70      75      80
Ser Ser Asn Leu Leu Ser Ala Asn Ile Ile Asn Gly Ala Thr Ile Glu
      85      90      95
Arg Glu Val Ser Tyr Asp Leu Phe His Lys Asn Ala Met Thr Leu Ser
      100     105     110
Leu Lys Asn Pro Asn Phe Lys Asn Ala Ile Gln Val Gln Asn Thr Leu
      115     120     125
Asn Lys Val Phe Gly Asn Lys Val Ala Ile Ala Leu Asp Pro Lys Thr
      130     135     140
Ile Gln Ile Thr Arg Pro Glu Arg Leu Ser Met Val Glu Phe Leu Ala
      145     150     155     160
Leu Val Gln Glu Ile Pro Ile Tyr Tyr Arg Ala Lys Asn Lys Ile Ile
      165     170     175
Val Asp Glu Lys Ser Gly Thr Ile Val Ser Gly Val Asp Ile Ile Val
      180     185     190
His Pro Ile Val Val Thr Ser Gln Asp Ile Thr Leu Lys Ile Thr Lys
      195     200     205
Glu Pro Leu Asn Asp Ser Lys Asn Met Gln Asp Leu Asp Asn Asn Met
      210     215     220
Ser Leu Asp Thr Ala His Asn Thr Leu Ser Ser Asn Gly Lys Asn Ile
      225     230     235     240
Thr Ile Ala Gly Val Val Lys Ala Leu Gln Lys Ile Gly Val Ser Ala
      245     250     255
Lys Gly Met Val Ser Ile Leu Gln Ala Leu Lys Lys Ser Gly Ala Ile
      260     265     270
Ser Ala Lys Trp Arg Tyr Tyr Asp Lys Gln Gln
      275     280

```

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502

```

Thr Gly His Gly Arg Leu Gly Trp Ile Leu Asn Pro Lys Lys Ala Lys
1      5      10      15
Phe Ile Ala Leu Lys Gln Ala Trp Ile Tyr Glu Arg Met Leu Ser Phe
      20      25      30
Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg Leu Thr Ala
      35      40      45
Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp Leu Glu Ile Gln
      50      55      60
Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys Ile Gln Ala Leu
65      70      75      80
Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys Val Val Ser Lys
      85      90      95
Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn Ala Asn Val Ser
      100      105      110
Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn Met Ser Leu Gly
      115      120      125
Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu Thr Gln Ser Lys
130      135      140
Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu Leu Lys Lys Thr
145      150      155      160
Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly Ile Glu Asn Tyr
      165      170      175
Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala Ile Lys Asn Leu
      180      185      190
Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser Pro Asp Leu Ile
195      200      205
Ala Ile Ala Lys Leu Glu Ile Leu Lys Ser Gln Leu Glu Ile
210      215      220

```

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503

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```

Ile Val Phe His Gln Gly Ser Leu Ser Val Ser Gly Leu Phe Lys Met
1      5      10      15
Arg Ile Leu Ser Phe Lys Lys Asn Lys Arg Ala Val Phe Ser Leu Tyr
20      25      30
Leu Phe Ile Ala Leu Leu Ala Leu Ser Leu Leu Ala Pro Leu Trp Val
35      40      45
Asn Asp Arg Pro Leu Phe Ile Tyr Lys Asp Asn Lys Ala Tyr Phe Pro
50      55      60
Met Phe Lys Asn Tyr Ala Glu Val Glu Phe Gly Gly Asp Phe Phe Thr
65      70      75      80
Pro Thr Asp Tyr Asn Asp Pro Tyr Val Gln Asn Thr Leu Leu Lys Asp
85      90      95
Ala Phe Ile Ile His Ala Leu Ile Pro Tyr Ser Tyr Asp Thr Ile Ile
100      105      110
Met Asp Leu Asp Ser Pro Ala Pro Thr Pro Pro Ser Phe Lys His Leu
115      120      125
Leu Gly Thr Asp Asp Gln Ala Arg Asp Val Leu Ala Arg Leu Val Tyr
130      135      140
Gly Tyr Arg Val Ser Leu Val Phe Gly Ile Leu Leu Thr Leu Phe Ser
145      150      155      160
Val Leu Ile Gly Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly
165      170      175
Leu Val Asp Leu Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile
180      185      190
Pro Met Leu Phe Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn
195      200      205
Phe Trp Ile Ile Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu
210      215      220
Ser Gln Val Val Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr
225      230      235      240
Thr Lys Ala Ala Arg Ala Leu Gly Val Asn Asp Leu Lys Ile Ile Phe
245      250      255
Tyr His Val Leu Pro Asn Ala Leu Val Ala Thr Ile Thr Tyr Ile Pro
260      265      270
Phe Leu Met Ala Ala Ser Ile Ser Thr Leu Val Ser Leu Asp Phe Leu
275      280      285
Gly Phe Gly Met Pro Ile Gly Ser Ala Ser Leu Gly Glu Leu Val Asn
290      295      300
Gln Gly Lys Asp Asn Leu Thr Thr Pro His Leu Ala Val Val Ala Phe
305      310      315      320
Val Ala Ile Ser Leu Leu Leu Ser Val Leu Val Phe Ile Gly Glu Gly
325      330      335
Val Arg Asp Ala Phe Asn Ala Asn Met Leu Lys
340      345

```

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504

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Arg Gly Tyr Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser
 1 5 10 15
 His Phe Ser Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg
 20 25 30
 Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn
 35 40 45
 Leu Val Met Arg Leu Asn Pro Arg Phe Lys Pro His Asn Gly Glu Ile
 50 55 60
 Leu Phe Glu Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Met Gln
 65 70 75 80
 His Leu Arg Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser
 85 90 95
 Ser Leu Asn Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr
 100 105 110
 Phe Leu His His Lys Asn Ala Ser Gln Val Leu Leu Lys Glu Gln Val
 115 120 125
 Leu Asn Ala Met Lys Gln Val Gln Leu Asp Glu Lys Phe Leu Asp Arg
 130 135 140
 Tyr Pro Tyr Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Cys Ile Ala
 145 150 155 160
 Met Gly Ile Ile Asn Ala Pro Lys Leu Leu Ile Cys Asp Glu Pro Thr
 165 170 175
 Thr Ala Leu Asp Ala Gln Ile Gln Asn Gln Ile Leu Asp Leu Leu Lys
 180 185 190
 Gln Leu Ser Val Glu Lys Asn Ile Ala Leu Leu Phe Ile Ser His Asp
 195 200 205
 Leu Lys Ala Val Lys Arg Leu Ala Asp Arg Val Tyr Val Leu Lys Lys
 210 215 220
 Gly Glu Ile Val Glu Thr Asn Leu Thr Lys Glu Leu Phe Asn Asp Pro
 225 230 235 240
 Lys His Glu Tyr Ser Lys Leu Leu Ile Gln Ala Ser Asn Leu Pro Ala
 245 250 255
 Lys Asn Leu Lys Ala Leu Asp Glu Thr Leu Leu Glu Val Lys Asp Phe
 260 265 270
 Ser Val Tyr Tyr Leu Gln Lys Arg Phe Phe Arg Pro Ser Leu Lys Lys
 275 280 285
 Pro Leu Ile Ala Ser Val Asp Phe Ser Leu Lys Ala Lys Glu Asn Ile
 290 295 300
 Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Ser Leu Ala Leu Gly
 305 310 315 320
 Leu Leu Lys Leu Ala Leu Asn Ser Gly Glu Glu Lys Ile Leu Gly Gln
 325 330 335
 Ser Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile
 340 345 350
 Leu Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu
 355 360 365
 Ser Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys
 370 375 380
 Ala Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu
 385 390 395 400
 Val Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser
 405 410 415
 Gly Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys
 420 425 430
 Pro Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser
 435 440 445
 Ile Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln
 450 455 460
 Asp Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala
 465 470 475 480
 Phe Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr
 485 490 495
 Gly Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys
 500 505 510

1065

Arg Leu Leu Glu Ser Arg Leu
515

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Leu | Met | Asn | Thr | Ile | Ile | Arg | Tyr | Ala | Ser | Leu | Trp | Gly | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Cys | Ile | Thr | Leu | Thr | Leu | Ala | Gln | Thr | Pro | Ser | Lys | Thr | Pro | Asp | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Lys | Gln | Ile | Leu | Asn | Asn | Tyr | Ser | His | Lys | Asn | Leu | Lys | Leu | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Pro | Pro | Thr | Ser | Ser | Leu | Glu | Ala | Thr | Pro | Gly | Phe | Leu | Pro | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Lys | Glu | Thr | Ala | Thr | Thr | Ile | Asn | Gln | Glu | Ile | Ala | Lys | Tyr | His |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Glu | Lys | Ser | Asp | Lys | Ala | Ala | Leu | Gly | Leu | Tyr | Glu | Leu | Leu | Lys | Gly |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Thr | Thr | Asn | Leu | Ser | Leu | Gln | Ala | Gln | Glu | Leu | Ser | Val | Lys | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Met | Lys | Asn | His | Thr | Ile | Ala | Lys | Ala | Met | Phe | Leu | Pro | Thr | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asn | Ala | Ser | Tyr | Asn | Phe | Lys | Asn | Glu | Ala | Arg | Asp | Thr | Pro | Glu | Tyr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | His | Tyr | Asn | Thr | Gln | Gln | Leu | Gln | Ala | Gln | Val | Thr | Leu | Asn | Val |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Phe | Asn | Gly | Phe | Ser | Asn | Val | Asn | Asn | Val | Lys | Glu | Lys | Ser | Ala | Thr |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Thr | Asp | Pro | Leu | Trp | Leu | Ile | | | | | | | | | |
| | | | 180 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506

```

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1      5      10      15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
20     25     30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
35     40     45
Ala Asp His Thr Leu Ile Gly Gly Ala Gly Gln Ile Leu Asp Pro
50     55     60
Glu Met Ile Glu Asn Ala Leu His Ser Val Lys Asn Pro Lys His Thr
65     70     75     80
Ile Phe Leu Ser Ala Val Gly Lys Pro Phe Lys Gln Ile Asp Ala Met
85     90     95
Arg Leu Ala Gln Lys Lys His Val Val Leu Val Cys Gly Arg Tyr Glu
100    105    110
Gly Phe Asp Glu Arg Ser Ile Glu Leu Gly Ala Asp Glu Val Phe Cys
115    120    125
Ile Gly Asp Phe Ile Leu Thr Gly Gly Glu Leu Gly Ala Leu Cys Leu
130    135    140
Ile Asp Ser Ile Ala Arg His Ile Gln Gly Val Leu Gly Asn Ala Gln
145    150    155    160
Ser Leu Glu Asn Glu Ser Phe Glu Asn Asn Tyr Leu Glu Thr Pro Asn
165    170    175
Phe Ala Asn Ala Val Phe Lys Ser Lys Glu Ile Asn Lys Ile Pro Ala
180    185    190
Pro Leu Glu Tyr Ser Lys Gly Asn His Ala Lys Ile Lys Gln Leu Lys
195    200    205
Leu Asp Leu Ser Lys Leu Arg Thr Lys Phe Tyr Arg Leu Asp Leu Phe
210    215    220
Lys Gln His Lys Ser
225

```

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507

```

Arg Glu Gln Trp Phe His Phe Arg Ser Thr Pro Pro Thr Val Val Leu
1      5      10      15
Met Ala Gly Leu Gln Gly Ser Gly Lys Thr Thr Thr Thr Ala Lys Leu
20     25     30
Ala His Tyr Leu Lys Thr Lys Asn Lys Lys Val Leu Leu Cys Ala Cys
35     40     45
Asp Leu Gln Arg Leu Ala Ala Val Glu Gln Leu Lys Val Leu Gly Glu
50     55     60

```

SUBSTITUTE SHEET (RULE 26)

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Gln Val Gly Val Glu Val Phe His Glu Glu Asn Lys Ser Val Lys Glu
 65 70 75 80
 Ile Ala Asn Asn Ala Leu Lys Arg Ala Lys Glu Ala Gln Phe Asp Val
 85 90 95
 Leu Ile Val Asp Ser Ala Gly Arg Leu Ala Ile Asp Lys Glu Leu Met
 100 105 110
 Gln Glu Leu Lys Glu Val Lys Glu Val Leu Asn Pro His Glu Val Leu
 115 120 125
 Tyr Val Ala Asp Ala Leu Ser Gly Gln Asp Gly Val Lys Ser Ala Asn
 130 135 140
 Thr Phe Asn Glu Glu Ile Gly Val Ser Gly Val Val Leu Ser Lys Phe
 145 150 155 160
 Asp Ser Asp Ser Lys Gly Gly Ile Ala Leu Gly Ile Thr Tyr Gln Leu
 165 170 175
 Gly Leu Pro Leu Arg Phe Ile Gly Ser Gly Glu Lys Ile Pro Asp Leu
 180 185 190
 Asp Val Phe Met Pro Glu Arg Ile Val Gly Arg Leu Met Gly Ala Gly
 195 200 205
 Asp Ile Ile Ser Leu Ala Glu Lys Thr Ala Ser Val Leu Asn Pro Asn
 210 215 220
 Glu Ala Lys Asp Leu Ser Lys Lys Leu Lys Lys Gly Gln Phe Thr Phe
 225 230 235 240
 Asn Asp Phe Leu Asn Gln Ile Glu Lys Val Lys Lys Leu Gly Ser Met
 245 250 255
 Ser Ser Leu Ile Ser Met Ile Pro Gly Leu Gly Asn Met Ala Ser Ala
 260 265 270
 Leu Lys Asp Thr Asp Leu Glu Ser Ser Leu Glu Val Lys Lys Ile Lys
 275 280 285
 Ala Met Val Asn Ser Met Thr Lys Lys Glu Arg Glu Asn Pro Glu Ile
 290 295 300
 Leu Asn Gly Ser Arg Arg Lys Arg Ile Ala Leu Gly Ser Gly Leu Glu
 305 310 315 320
 Val Ser Glu Ile Asn Arg Ile Ile Lys Arg Phe Asp Gln Ala Ser Lys
 325 330 335
 Met Ala Lys Arg Leu Thr Asn Lys Lys Gly Ile Ser Asp Leu Met Asn
 340 345 350
 Leu Met Ser Gln Ala Lys Asn Gln Thr Pro Pro Lys Met Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508

Arg Lys Ala Met Asn Thr His Leu Lys Gln Leu Ile Glu Ile Ser His
 1 5 10 15
 Leu Asp Lys Glu Ile Asp Ser Leu Glu Pro Leu Ile Arg Glu Lys Arg
 20 25 30
 Lys Asp Leu Asp Lys Ala Leu Asn Asp Lys Glu Ala Lys Asn Lys Ala

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```

      35      40      45
Ile Leu Asn Leu Glu Glu Glu Lys Leu Ala Leu Lys Leu Gln Val Ser
  50      55      60
Lys Asn Glu Gln Thr Leu Gln Asp Thr Asn Ala Lys Ile Ala Ser Ile
  65      70      75      80
Gln Lys Lys Met Ser Glu Ile Lys Ser Glu Arg Glu Leu Arg Ser Leu
      85      90      95
Asn Ile Glu Glu Asp Ile Ala Lys Glu Arg Ser Asn Gln Ala Asn Arg
      100      105      110
Glu Ile Glu Asn Leu Gln Asn Glu Ile Lys His Lys Ser Glu Lys Gln
      115      120      125
Glu Val Leu Lys Lys Glu Met Leu Glu Leu Glu Lys Leu Ala Leu Glu
      130      135      140
Leu Glu Asn Leu Val Glu Asn Glu Val Lys Asn Ile Lys Glu Thr Gln
      145      150      155      160
Gln Ile Ile Phe Lys Lys Lys Glu Glu Leu Val Glu Lys Thr Glu Pro
      165      170      175
Lys Ile Tyr Ser Phe Tyr Glu Arg Ile Arg Arg Trp Ala Lys Asn Thr
      180      185      190
Ser Ile Val Thr Ile Lys Lys Gln Ala Cys Gly Gly Cys Phe Ile Arg
      195      200      205
Leu Asn Asp Lys Ile Tyr Ala Glu Val Leu Thr Ser Gly Asp Met Ile
      210      215      220
Thr Cys Pro Tyr Cys Gly Arg Ile Leu Tyr Ala Glu Ser Thr His Glu
      225      230      235      240
Ser Asn Ala Gln Pro Pro Lys Glu Ser Gln Pro Lys Glu Ser Gln Glu
      245      250      255
Glu Ser Gln Glu Glu Ser Gln Glu Glu Ser Gln Glu Ser Val
      260      265      270

```

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509

```

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
  1      5      10      15
Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
      20      25      30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
      35      40      45
Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
      50      55      60
Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
      65      70      75      80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
      85      90      95
Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val
      100      105      110

```

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Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
 115 120 125
 Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
 130 135 140
 Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
 145 150 155 160
 Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
 165 170 175
 Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
 180 185 190
 Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
 195 200 205
 Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
 210 215 220
 Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Lys Leu
 225 230 235 240
 Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
 245 250 255
 Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
 260 265 270
 Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
 275 280 285
 Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
 290 295 300
 Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
 305 310 315 320
 Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr
 325 330 335
 Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu Val Gln Ile
 340 345 350
 Arg Thr Phe Asp Met His Met Gly Ala Glu Tyr Gly Asn Ser Ala His
 355 360 365
 Trp Lys Tyr Lys Ala Gly Gly Val Asp His Glu Glu His His Glu Gly
 370 375 380
 Met Arg Trp Leu Gln Asn Phe Lys Tyr His Asp Ser Asp Leu Lys Asn
 385 390 395 400
 Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys Asn Asp Leu Tyr Arg Glu
 405 410 415
 Asp Ile Val Val Phe Ser Pro His Gly Asp Thr Tyr Thr Leu Pro Val
 420 425 430
 Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met Val His Ser Asp Leu Gly
 435 440 445
 Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser Lys Lys Ala Leu Leu Asn
 450 455 460
 Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys Gly Asp Lys
 465 470 475 480
 Val Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr Ser Lys Ala
 485 490 495
 Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys Glu Ile Asp
 500 505 510
 Thr Lys Ser Met Ile Asn Ile Leu Ser Thr Phe Phe Gly Arg Ser Val
 515 520 525
 Phe Glu Asp Ala Asp Leu Lys Asp Tyr Lys Asn Phe Glu Glu Lys Leu
 530 535 540
 Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met Lys Ser Phe
 545 550 555 560
 Glu Asn Leu Gly Gln Thr His
 565

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510

```

Val Thr Ile Lys Ser Phe Ile Asn Gly Leu Arg Arg Asp His Ala Gly
1          5          10          15
Lys Asp Lys Lys Gln Ala Gly Phe Gly Glu Ile Phe Trp Gly Ser Val
20          25          30
Ser Trp Gly Gln Pro Val Trp Ile Asp Ile His Val Leu Asp His Ile
35          40          45
Ala Lys Glu Ile Arg Ser Leu Val Glu Asn Asp Ile Glu Val Gly Ile
50          55          60
Val Ile Gly Gly Gly Asn Ile Ile Arg Gly Val Ser Ala Ala Gln Gly
65          70          75          80
Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr Met Gly Met Leu Ala Thr
85          90          95
Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His Ile Gly Leu
100         105         110
Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile Cys Glu Ser
115         120         125
Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly Arg Val Val
130         135         140
Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr Asp Thr Ala
145         150         155         160
Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile Ile Lys Ala
165         170         175
Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys Phe Lys Asp
180         185         190
Ala Lys Asn Trp Thr Leu
195

```

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511

```

Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1          5          10          15

```

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Thr Asp Asp Leu Ser Pro Ala Ser Asp Ala Phe Thr Arg Ser Asp Ile
 20 25 30
 Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
 35 40 45
 Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
 50 55 60
 Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
 65 70 75 80
 Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
 85 90 95
 Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
 100 105 110
 Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
 115 120 125
 Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
 130 135 140
 Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
 145 150 155 160
 Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
 165 170 175
 Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Leu Gly Glu Ser
 180 185 190
 Glu Ala Phe Lys Lys Pro Ser Ala Pro Lys Ser Asp Ala Lys Gly Tyr
 195 200 205
 Thr Leu Ala Gln Lys Ile Val Gly His Ala Cys Gly Val Lys Gly Ile
 210 215 220
 Leu Pro Gly Ala Tyr Cys Glu Pro Lys Val Thr Thr Val Gly Ser Gln
 225 230 235 240
 Asp Thr Thr Gly Ala Met Thr Arg Asp Glu Val Lys Glu Leu Ala Ser
 245 250 255
 Leu Lys Phe Asp Ala Pro Phe Val Leu Gln Ser Phe Cys His Thr Ala
 260 265 270
 Ala Tyr Pro Lys Pro Ser Asp Val Ser Leu His Ala Thr Leu Pro Gly
 275 280 285
 Phe Ile Thr Gln Arg Gly Gly Val Ala Leu His Pro Gly Asp Gly Val
 290 295 300
 Ile His Thr Trp Leu Asn Arg Met Gly Leu Pro Asp Thr Leu Gly Thr
 305 310 315 320
 Gly Gly Asp Ser His Thr Arg Phe Pro Leu Gly Ile Ser Phe Arg Gln
 325 330 335
 Gly Ala Gly

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512

Thr Phe Thr Ile Lys Arg Phe Val Leu Met Lys Ile Lys Ile Gln Lys

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```

1           5           10           15
Ile His Pro Asn Ala Leu Ile Pro Lys Tyr Gln Thr Glu Gly Ser Ser
                20           25           30
Gly Phe Asp Leu His Ala Val Glu Val Val Ile Lys Pro His Ser
                35           40           45
Val Gly Leu Val Arg Ile Gly Ile Cys Leu Ser Leu Glu Val Gly Tyr
                50           55           60
Glu Leu Gln Val Arg Thr Arg Ser Gly Leu Ala Leu Asn His Gln Val
65           70           75           80
Met Val Leu Asn Ser Pro Gly Thr Val Asp Asn Asp Tyr Arg Gly Glu
                85           90           95
Ile Lys Val Ile Leu Ala Asn Leu Ser Asp Lys Asp Phe Lys Val Gln
                100          105          110
Val Gly Asp Arg Ile Ala Gln Gly Val Val Gln Lys Thr Tyr Lys Ala
                115          120          125
Glu Phe Ile Glu Cys Glu Gln Leu Asp Glu Thr Ser Arg Gly Ser Gly
                130          135          140
Gly Phe Gly Ser Thr Gly Val Ser Lys Ala
145           150

```

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513

```

Arg Lys Lys Pro Phe Lys Glu Arg Ile Asp Leu Met Asn Lys Pro Phe
1           5           10           15
Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser Gly Cys Asn Met Arg
                20           25           30
Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe
                35           40           45
Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala
50           55           60
Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu
65           70           75           80
Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser
                85           90           95
Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys
                100          105          110
Lys Thr Ser Lys Ser Arg Ala Ala Lys Thr Glu Glu Thr Glu Leu Lys
                115          120          125
Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val
                130          135          140
Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile
145           150           155           160
Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
                165           170           175

```

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(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514

```

Gly Met Ser Ile Lys Glu Asn Leu Glu Gln Val Arg Asn Glu Phe Lys
1      5      10      15
Ser Asp Glu Lys Leu Leu Glu Gly Ala Phe Arg Leu Glu Lys Phe Phe
      20      25      30
Lys Arg Tyr Lys Trp Val Leu Leu Phe Ile Val Val Ala Phe Ile Ala
      35      40      45
Tyr Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Glu Gln Thr Arg
      50      55      60
Glu Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn
      65      70      75      80
Ile Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp
      85      90      95
Leu Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe
      100     105     110
Lys Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys
      115     120     125
Tyr Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser
      130     135     140
Pro Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr
      145     150     155     160
Glu Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser
      165     170     175
Thr Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys
      180     185     190
His Tyr Gly Met Leu Glu Asp Ile Gln Gln Asn Pro Ser Lys Pro Thr
      195     200     205
Asn Leu Lys Lys Glu Thr Ile Gln Gly Thr His
      210     215

```

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515

```

Lys Arg Tyr Lys Arg Leu Glu Gln Glu Ile Lys Lys Arg Asp Lys Met
1      5      10      15
Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu Ala
20     25     30
His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met Arg
35     40     45
Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile Leu
50     55     60
Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu Glu
65     70     75     80
Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val Gly
85     90     95
Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu Phe
100    105    110
Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val Pro
115    120    125
Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile Gly
130    135    140
Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe Leu
145    150    155    160
Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val Leu
165    170    175
Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu Ala
180    185    190
Leu Gln Gln Leu Arg Ser
195

```

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516

```

Ser Arg Thr Leu Cys Ala Lys Ile Val Leu Gln Lys Glu Arg Lys Lys
1      5      10      15
Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
20     25     30
Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
35     40     45
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
50     55     60
Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
65     70     75     80
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
85     90     95

```

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```

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
      100      105      110
Glu Tyr Asp Leu Tyr Lys Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
      115      120      125
Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
      130      135      140
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys
      145      150      155      160
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
      165      170      175
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
      180      185      190
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asn Phe Asn Ala
      195      200      205
Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
      210      215      220
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
      225      230      235      240
Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
      245      250      255
Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Asn Gly Asn
      260      265      270
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
      275      280      285
Tyr Ser Thr Ile Asn Thr Ser Lys Val Gln Gly Glu Val Asp Phe Asn
      290      295      300
His Leu Thr Val Gly Asp Gln Asn Ala Ala Gln Ala Gly Ile Ile Ala
      305      310      315      320
Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
      325      330      335
Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
      340      345      350
Ser Thr Thr Ser Gln Ser Gly Thr Lys Asn Asp Lys Lys Glu Ile Ser
      355      360      365
Gln Asn Asn Asn Ser Asn Thr Glu Val Ile Asn Pro Pro Asn Asn Thr
      370      375      380
Gln Lys Thr Glu Thr Glu Pro Thr Lys Ser Leu Met Gly Leu Leu Leu
      385      390      395      400
Lys Ala Lys Thr Arg Leu Ser
      405

```

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517

```

Val Ile Asn Thr Thr Ser Met Leu Lys Lys Ile Phe Leu Thr Asn Ser
1      5      10      15
Leu Gly Ile Leu Cys Ser Arg Ile Phe Gly Phe Leu Arg Asp Leu Met

```

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```

      20      25      30
Met Ala Asn Ile Leu Gly Ala Gly Val Tyr Ser Asp Ile Phe Phe Val
    35      40      45
Ala Phe Lys Leu Pro Asn Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser
    50      55      60
Phe Ser Gln Ser Phe Leu Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly
    65      70      75      80
Gly Phe Ala Ser Leu Val Gly Leu Ile Phe Cys Gly Val Leu Phe Met
    85      90      95
Trp Cys Leu Leu Val Ala Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu
    100      105      110
Ala Tyr Gly Phe Asp Glu Glu Thr Leu Lys Leu Cys Thr Pro Ile Val
    115      120      125
Ala Ile Asn Phe Trp Tyr Leu Leu Val Phe Ile Thr Thr Phe Leu
    130      135      140
Gly Ala Leu Leu Gln Tyr Lys His Ser Phe Phe Ala Ser Ala Tyr Ser
    145      150      155      160
Ala Ser Leu Leu Asn Leu Cys Met Ile Leu Ala Leu Leu Ile Ser Lys
    165      170      175
Glu Lys Thr His Leu Glu Ala Leu Tyr Tyr Leu Ser Tyr Gly Val Leu
    180      185      190
Leu Gly Gly Val Ala Gln Ile Leu Leu His Phe Tyr Pro Leu Val Lys
    195      200      205
Leu Gly Leu Trp Asp Leu Leu Phe Lys Gly Leu Leu Gly Phe Lys Thr
    210      215      220
Lys Asn Thr Asn Lys Lys Glu Tyr Arg Leu Asn Arg Ala Lys Lys Asp
    225      230      235      240
Leu Lys Ala Phe Phe Lys Gln Phe Phe Pro Ser Val Leu Gly Asn Ser
    245      250      255
Ser Ala Gln Ile Ala Ser Phe Leu Asp Thr Thr Ile Ala Ser Phe Leu
    260      265      270
Ala Ser Gly Ser Val Ser Tyr Leu Tyr Tyr Ala Asn Arg Val Phe Gln
    275      280      285
Leu Pro Leu Ala Leu Phe Ala Ile Ala Ile Ser Thr Ala Leu Phe Pro
    290      295      300
Ser Ile Ala Ile Ala Leu Lys Asn Asn Gln Gln Asp Leu Ile Leu Gln
    305      310      315      320
Arg Leu Gln Lys Ala Trp Phe Phe Leu Val Gly Val Leu Leu Leu Cys
    325      330      335
Ser Ile Gly Gly Ile Met Leu Ser Lys Glu Ile Thr Glu Leu Leu Phe
    340      345      350
Glu Arg Gly Gln Phe Ser Pro Lys Asp Thr Leu Ile Thr Ser Gln Val
    355      360      365
Phe Ser Leu Tyr Leu Leu Gly Leu Leu Pro Phe Gly Leu Thr Lys Leu
    370      375      380
Phe Ser Leu Trp Leu Tyr Ala Lys Leu Glu Gln Lys Lys Ala Ala Lys
    385      390      395      400
Ile Ser Leu Ile Ser Leu Phe Leu Gly Leu Ala Ala Ser Leu Ser Leu
    405      410      415
Met Pro Leu Leu Gly Val Leu Gly Leu Arg
    420      425

```

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518

```

Phe Arg Leu Pro Ser Pro Leu Thr Ser Ile Leu Met Arg Leu Asp Tyr
1          5          10          15
Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg Glu Lys Ala Lys Ala
20          25          30
Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys Met Val Val Ser Lys
35          40          45
Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile Glu Leu Ile Ala Pro
50          55          60
Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu
65          70          75          80
Asp His Phe Ile Asp Phe Lys Glu Lys Val Val Leu Asp Val Gly Ala
85          90          95
Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Lys
100          105          110
Val Leu Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys
115          120          125
Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe
130          135          140
Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile
145          150          155          160
Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro Leu Ser Gly Glu Phe
165          170          175
Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Thr Ile Lys Arg
180          185          190
Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala Ile Leu Asn Ala Leu
195          200          205
Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Thr
210          215          220
Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe
225          230          235          240
Ile His Phe Lys Arg Ala
245

```

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519

```

Arg His Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile
1          5          10          15
Ile Gly Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn

```

SUBSTITUTE SHEET (RULE 26)

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ser | Gly | Leu | Val | Gly | Arg | Phe | Gly | Val | Trp | Phe | Ala | Ala | Ile | Asn | Lys | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Lys | Tyr | Phe | Gly | Tyr | Leu | Ser | Leu | Ile | Asn | Leu | Pro | Tyr | Leu | Ala | Trp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Val | Leu | Phe | Leu | Leu | Tyr | Arg | Ala | Lys | Asn | Pro | Phe | Thr | Glu | Ile | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Glu | Lys | Thr | Leu | Gly | His | Leu | Leu | Gly | Ile | Leu | Ser | Leu | Leu | Phe | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Gln | Ser | Ser | Leu | Leu | Asn | Gln | Gly | Glu | Ile | Gly | Asn | Ser | Ala | Arg | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Leu | Phe | Leu | His | Pro | Phe | Ile | Gly | Asp | Phe | Gly | Leu | Tyr | Val | Leu | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Met | Leu | Met | Val | Val | Ile | Ser | Tyr | Leu | Ile | Leu | Phe | Lys | Leu | Pro | Pro | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Lys | Ser | Val | Phe | Tyr | Pro | Tyr | Met | Asn | Lys | Thr | Gln | Ser | Leu | Leu | Lys | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Glu | Ile | Tyr | Lys | Gln | Cys | Leu | Gln | Ala | Phe | Ser | Pro | Asn | Phe | Ser | Leu | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| Lys | Lys | Glu | Gly | Phe | Glu | Asn | Thr | Pro | Ser | Asp | Ser | Gln | Lys | Lys | Glu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Thr | Asn | Asn | Asp | Lys | Glu | Lys | Glu | Asn | Leu | Lys | Glu | Asn | Pro | Ile | Asp | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Glu | Asn | His | Asn | Thr | Pro | Asn | Glu | Glu | Ser | Phe | Leu | Ala | Ile | Pro | Thr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Tyr | Asn | Thr | Thr | Leu | Asn | Asn | Ser | Glu | Pro | Gln | Glu | Gly | Leu | Val | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Gln | Ile | Ser | Pro | His | Pro | Pro | Thr | His | Tyr | Thr | Ile | Tyr | Pro | Lys | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Asn | Arg | Phe | Asp | Asp | Leu | Thr | Asn | Pro | Thr | Leu | Lys | Glu | Pro | Lys | Gln | |
| | | 260 | | | | | | 265 | | | | | 270 | | | |
| Glu | Thr | Lys | Glu | Arg | Glu | Pro | Thr | Leu | Lys | Lys | Glu | Thr | Pro | Thr | Thr | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Leu | Lys | Pro | Ile | Met | Pro | Ile | Ser | Ala | Ser | Asn | Thr | Glu | Asn | His | Asp | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Lys | Thr | Glu | Asn | His | Lys | Thr | Pro | Asn | His | Pro | Ile | Lys | Glu | Asp | Asp | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Leu | Gln | Glu | Ser | Pro | Gln | Glu | Asn | Pro | Gln | Lys | Glu | Asn | Ile | Glu | Glu | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Asn | Ile | Glu | Glu | Lys | Glu | Thr | Gln | Asn | Ala | Pro | Ser | Phe | Ser | Pro | Leu | |
| | | 340 | | | | | | 345 | | | | | 350 | | | |
| Thr | Leu | Thr | Ser | Ala | Lys | Lys | Pro | Val | Met | Val | Lys | Glu | Leu | Ser | Glu | |
| | | 355 | | | | | 360 | | | | | | | | | |

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Gly Lys Ser Val Gly Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys
 545 550 555 560
 Asn Pro Pro Asp Gln Leu Lys Leu Val Met Ile Asp Pro Lys Met Val
 565 570 575
 Glu Phe Ser Ile Tyr Ala Asp Ile Pro His Leu Leu Thr Pro Ile Ile
 580 585 590
 Thr Asp Pro Lys Lys Ala Ile Gly Ala Leu Gln Ser Val Ala Lys Glu
 595 600 605
 Met Glu Arg Arg Tyr Ser Leu Met Ser Glu Tyr Lys Val Lys Thr Ile
 610 615 620
 Asp Ser Tyr Asn Glu Gln Ala Gln Ser Asn Gly Val Glu Ala Phe Pro
 625 630 635 640
 Tyr Leu Ile Val Val Ile Asp Glu Leu Ala Asp Leu Met Met Thr Gly
 645 650 655
 Gly Lys Glu Ala Glu Phe Pro Ile Ala Arg Ile Ala Gln Met Gly Arg
 660 665 670
 Ala Ser Gly Leu His Leu Ile Val Ala Thr Gln Arg Pro Ser Val Asp
 675 680 685
 Val Val Thr Gly Leu Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe
 690 695 700
 Arg Val Gly Thr Lys Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly
 705 710 715 720
 Ala Gln Ser Leu Leu Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly
 725 730 735
 Thr Asn Gly Leu Val Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu
 740 745 750
 Ile Lys Lys Ile Val Asp Phe Ile Lys Ala Gln Lys Glu Val Glu Tyr
 755 760 765
 Asp Lys Asp Phe Leu Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro
 770 775 780
 Asn Tyr Gln Gly Asp Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu
 785 790 795 800
 Glu Lys Lys Ile Thr Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile
 805 810 815
 Gly Tyr Asn Gln Ala Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly
 820 825 830
 Phe Leu Ser Pro Arg Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn
 835 840 845
 Phe

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520

Asn Tyr Leu Lys Ile Ser Cys Ser Arg Ile Ala Met Asn Pro Gln Ile
 1 5 10 15
 Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu Leu Ala Ala Ser Ser

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| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | | | | 20 | | | | | | 25 | | | | | 30 | | | | |
| Gly | Asn | Leu | Val | Glu | Trp | Tyr | Asp | Phe | Tyr | Ala | Tyr | Ala | Phe | Leu | Ala | | | | |
| | 35 | | | | | | 40 | | | | | 45 | | | | | | | |
| Pro | Tyr | Phe | Ala | Lys | Glu | Phe | Thr | His | Thr | Asn | Asp | Pro | Thr | Leu | Ala | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | | |
| Leu | Ile | Ser | Ala | Phe | Leu | Val | Phe | Met | Leu | Gly | Phe | Phe | Met | Arg | Pro | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| Leu | Gly | Ser | Leu | Phe | Phe | Gly | Lys | Leu | Gly | Asp | Lys | Lys | Gly | Arg | Lys | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | |
| Thr | Ser | Met | Val | Tyr | Ser | Ile | Ile | Leu | Met | Ala | Leu | Gly | Ser | Phe | Met | | | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | | | |
| Leu | Ala | Leu | Leu | Pro | Thr | Lys | Glu | Ile | Val | Gly | Glu | Trp | Ala | Phe | Leu | | | | |
| | 115 | | | | | | 120 | | | | | 125 | | | | | | | |
| Phe | Leu | Leu | Leu | Ala | Arg | Leu | Gln | Gly | Phe | Ser | Val | Gly | Gly | Glu | | | | | |
| | 130 | | | | | 135 | | | | 140 | | | | | | | | | |
| Tyr | Gly | Val | Val | Ala | Thr | Tyr | Leu | Ser | Glu | Leu | Gly | Lys | Asn | Gly | Lys | | | | |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | | | | | |
| Lys | Gly | Phe | Tyr | Gly | Ser | Phe | Gln | Tyr | Val | Thr | Leu | Val | Gly | Gly | Gln | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | |
| Leu | Leu | Ala | Ile | Phe | Ser | Leu | Phe | Ile | Val | Glu | Asn | Val | Tyr | Thr | His | | | | |
| | | | 180 | | | | | 185 | | | | | | 190 | | | | | |
| Glu | Gln | Ile | Ser | Ala | Phe | Ala | Trp | Arg | Tyr | Leu | Phe | Ala | Leu | Glu | Gly | | | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | | | |
| Ile | Leu | Ala | Leu | Leu | Ser | Leu | Phe | Leu | Arg | Asn | Ile | Met | Glu | Glu | Thr | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | | |
| Met | Asp | Asn | Glu | Ala | Thr | Pro | Gln | Lys | Lys | Thr | Asn | Val | Asn | Asn | Thr | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | | | | | |
| Lys | Glu | Thr | His | Ile | Lys | Glu | Thr | Gln | Arg | Gly | Ser | Leu | Lys | Glu | Leu | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | |
| Leu | Asn | His | Lys | Lys | Ala | Leu | Met | Ile | Val | Phe | Gly | Leu | Thr | Met | Gly | | | | |
| | | | 260 | | | | | 265 | | | | | | 270 | | | | | |
| Gly | Ser | Leu | Cys | Phe | Tyr | Thr | Phe | Thr | Val | Tyr | Leu | Lys | Ile | Phe | Leu | | | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | | | |
| Thr | Asn | Ser | Ser | Ser | Phe | Ser | Pro | Lys | Glu | Ser | Ser | Phe | Ile | Met | Leu | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | |
| Leu | Ala | Leu | Ser | Tyr | Phe | Ile | Phe | Leu | Gln | Pro | Leu | Cys | Gly | Met | Leu | | | | |
| 305 | | | | | 310 | | | | | | | | | | | | | | |

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521

Lys Trp Lys Asn Leu Met Gln Leu Ser Asn Ala Asp Leu Glu Arg Leu
 1 5 10 15
 Lys Ser Met Ala Asn Thr Leu Arg Phe Leu Cys Ala Asp Met Ile Asp
 20 25 30
 Lys Ala Asn Ser Gly His Pro Gly Val Cys Leu Gly Leu Ala Asp Val
 35 40 45
 Met Val Val Leu Ser Leu His Leu Asn Leu Asn Pro Thr Asn Pro Lys
 50 55 60
 Trp Leu Asn Arg Asp Arg Leu Val Phe Ser Gly Gly His Ala Ser Ala
 65 70 75 80
 Leu Val Tyr Ser Leu Leu His Leu Trp Gly Phe Asp Leu Ser Leu Asp
 85 90 95
 Asp Leu Lys Arg Phe Arg Gln Leu His Ser Lys Thr Pro Gly His Pro
 100 105 110
 Glu Leu His His Thr Glu Gly Ile Glu Ile Thr Thr Ala Pro Leu Gly
 115 120 125
 Gln Gly Phe Ala Asn Ala Val Gly Phe Ser Met Ala Ser Gln Tyr Ala
 130 135 140
 Gln Thr Leu Leu Asp Lys Glu Ala Ile Ser His Lys Val Tyr Cys Leu
 145 150 155 160
 Cys Gly Asp Gly Asp Leu Gln Glu Gly Ile Ser Tyr Glu Ser Thr Ser
 165 170 175
 Leu Ala Gly His Leu Arg Leu Asp Asn Leu Ile Val Ile Tyr Asp Ser
 180 185 190
 Asn Gln Ile Ser Ile Glu Gly Ala Ile Asn Ile Ser Phe Ser Glu Gln
 195 200 205
 Val Lys Thr Arg Phe Leu Ala Gln Asn Trp Glu Val Leu Glu Cys Asp
 210 215 220
 Gly His Asp Tyr Gln Ala Ile His Asn Ala Leu Glu Glu Ala Lys Lys
 225 230 235 240
 Ser His Lys Pro Thr Leu Leu Ile Ala His Thr Ile Ile Gly Lys Gly
 245 250 255
 Ala Ile Gly Leu Glu Gly Ser Glu Lys Thr His Gly Ser Pro Leu Ser
 260 265 270
 Lys Glu Val Leu Lys Gln Ser Lys Glu Asn Ala Gln Ile Asn Pro Asn
 275 280 285
 Glu Ser Phe Ile Ile Ser Pro Lys Asn Lys Met His Phe Glu Glu Val
 290 295 300
 Lys Val Arg Gly Ile Ser Leu Glu Ala Leu Trp Glu Lys Ser Leu Ser
 305 310 315 320
 Pro Lys Thr Lys Glu Lys Ile His Ala Leu Lys Asn Phe Asp Phe Asn
 325 330 335
 Ala Ile Asn Tyr Pro Ala Phe Lys Lys Gly Glu Ser Leu Ala Thr Arg
 340 345 350
 Val Ser Asn Gly Met Ile Leu Asn Ala Ile Ala Lys Glu Cys Glu Gly
 355 360 365
 Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser Asn Asn Thr His Leu
 370 375 380
 Lys His Ser Gly Asp Phe Pro Leu Gly Gln Asn Leu His Phe Gly Ile
 385 390 395 400
 Arg Glu His Ala Met Gly Ala Ile Thr Asn Ala Leu Ala Ala Tyr Gly
 405 410 415
 Leu Phe Val Pro Phe Cys Ala Thr Phe Phe Val Phe Ser Asp Tyr Leu
 420 425 430
 Met Pro Ser Ile Arg Leu Ser Ala Leu Met Lys Leu Lys Ala Leu Phe

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      435              440              445
Ile Phe Thr His Asp Ser Ile Gly Val Gly Glu Asp Gly Ala Thr His
  450              455              460
Gln Pro Ile Glu Gln Leu Ser His Leu Arg Ala Leu Pro His Phe Tyr
  465              470              475              480
Ala Phe Arg Pro Ser Asp Ala Phe Glu Asn Lys Ala Cys Met Gln Val
      485              490              495
Ala Leu Ser Leu Asn Ala Pro Ser Ala Leu Ile Leu Ser Arg Gln Asn
      500              505              510
Leu Ser Val Leu Asp Glu Val Ser Lys Glu Gln Val Leu Lys Gly Ala
      515              520              525
Tyr Val Lys His His Ser Lys Asp Pro Ile Ile Thr Leu Val Ala Ser
      530              535              540
Gly Ser Glu Val Ser Leu Ala Leu Glu Ser Ala Lys Ile Leu Glu Arg
  545              550              555              560
Glu Asn Ile Pro Thr Gln Val Val Ser Ala Pro Cys Phe Asp Leu Leu
      565              570              575
Val Glu Gln Asp Glu Ser Tyr Phe Lys Glu Leu Phe Lys Gly Lys Val
      580              585              590
Leu Val Ile Glu Ala Ser Arg Ala Ile Glu Trp Tyr Arg Phe Ala Asp
      595              600              605
Lys Ile Ile Gly Met Asp Ser Phe Gly Ser Ser Ala Lys Gly Asp Lys
      610              615              620
Leu Phe Glu Lys Phe Gly Phe Ser Val Glu Asn Ile Thr Ala Gln Ala
  625              630              635              640
Lys Arg Leu Leu Asn Ala
      645

```

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522

```

Lys Asp Tyr Cys Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met
  1              5              10              15
Ala Thr Gln Phe Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn
      20              25              30
Leu Asn Thr Asn Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe
      35              40              45
Leu Arg Leu Tyr Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln
      50              55              60
Thr Lys Ala Ser Ala Lys Tyr Leu Asn Arg Asn Leu Asn Arg Val Pro
  65              70              75              80
Ile Leu Ser Glu Ile Tyr Thr Asp Arg Ser Leu Gly Ala Phe Glu Gly
      85              90              95
Thr Asn Asn Pro Leu Asp Phe Ala Leu Thr Ser Pro Asn Leu Tyr Phe
      100              105              110
Ala Ile Gln Thr Asn Glu Gly Val Ala Tyr Thr Lys Asp Gly His Phe
      115              120              125

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```

Ser Val Asp Lys Asp Gly Phe Leu Val Thr Leu Asn Gly Phe Lys Val
 130          135          140
Leu Ser Arg Ser Gly Leu Asn Glu Lys Gly Gly Ile Met Leu Met Pro
145          150          155          160
Asn Ala Glu Ile Glu Val Asp Gln Asn Gly Gly Ile Thr Phe Arg Asp
          165          170          175
Asn Glu Ala Gln Ile Gln Ala Gly Ala Leu Ala Leu Val Ser Phe Ser
          180          185          190
Glu Pro Lys Asn Leu Lys Lys Ile Gly Gln Asn Leu Tyr Thr Tyr Gln
          195          200          205
Gly Glu Gly Val His Gln Val Ser Asp Ser Gly Ala Leu Arg Gln Ser
          210          215          220
Met Leu Glu Lys Ser Asn Val Asn Ala Val Arg Glu Met Ser Thr Leu
225          230          235          240
Ile Glu Ile Asn Arg Phe Leu Asp Met Tyr Ser Lys Val Leu Lys Thr
          245          250          255
His Gln Asp Asp Met Asn Ala Glu Ala Ile Asn Lys Leu Ala Thr Lys
          260          265          270
Ala

```

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523

```

Gly Met Ile Ala Leu Asn Phe Asn Leu Leu Asp Lys Glu Thr Asn Thr
 1          5          10          15
Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu Leu Tyr Lys
          20          25          30
Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr Phe Gly Leu
          35          40          45
Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu Asn Leu Lys
          50          55          60
Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe Ile Val Leu
          65          70          75          80
Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg Leu Ile Leu
          85          90          95
Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser Leu Phe Asp
          100          105          110
Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp Leu Lys Leu
          115          120          125
Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile Glu Ile Asn
          130          135          140
Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser Val Gly Asn
          145          150          155          160
Asp Ala Lys Asp Ala Leu Ile Gly Ile Lys Gln His Val Ala Asn Leu
          165          170          175
Pro Glu Val Ile Lys Ser Pro Ser Leu Val Asp Phe Val Asn Ala Leu

```

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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 180 | | | | | | | | | | 185 | | | | | | | | | | 190 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Asn | Arg | Asp | Thr | Ala | Ile | Ile | Val | Ser | Thr | Gly | Pro | Ser | Leu | Asn | Lys | Asn | Arg | Asp | Thr | Ala | Ile | Ile | Val | Ser | Thr | Gly | Pro | Ser | Leu | Asn | Lys | Asn | Arg | Asp | Thr | Ala | Ile | Ile | Val | Ser | Thr | Gly | Pro | Ser | Leu | Asn |
| 195 | | | | | | | | | | 200 | | | | | | | | | | 205 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Gln | Leu | Pro | Leu | Leu | Lys | Glu | Ile | Ala | Pro | Tyr | Ala | Thr | Leu | Phe | Lys | Gln | Leu | Pro | Leu | Leu | Lys | Glu | Ile | Ala | Pro | Tyr | Ala | Thr | Leu | Phe | Lys | Gln | Leu | Pro | Leu | Leu | Lys | Glu | Ile | Ala | Pro | Tyr | Ala | Thr | Leu | Phe |
| 210 | | | | | | | | | | 215 | | | | | | | | | | 220 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Cys | Ile | Asp | Ala | Ser | Phe | Pro | Ile | Leu | Ala | Arg | Ala | Gly | Ile | Lys | Pro | Cys | Ile | Asp | Ala | Ser | Phe | Pro | Ile | Leu | Ala | Arg | Ala | Gly | Ile | Lys | Pro | Cys | Ile | Asp | Ala | Ser | Phe | Pro | Ile | Leu | Ala | Arg | Ala | Gly | Ile | Lys | Pro |
| 225 | | | | | | | | | | 230 | | | | | | | | | | 235 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asp | Ile | Val | Leu | Ser | Leu | Glu | Arg | Val | Asp | Leu | Thr | Ala | Lys | Phe | Tyr | Asp | Ile | Val | Leu | Ser | Leu | Glu | Arg | Val | Asp | Leu | Thr | Ala | Lys | Phe | Tyr | Asp | Ile | Val | Leu | Ser | Leu | Glu | Arg | Val | Asp | Leu | Thr | Ala | Lys | Phe | Tyr |
| 245 | | | | | | | | | | 250 | | | | | | | | | | 255 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu | Glu | Thr | Pro | Leu | Asp | Phe | Gln | Glu | Gly | Val | Ile | Phe | Ala | Leu | Thr | Glu | Glu | Thr | Pro | Leu | Asp | Phe | Gln | Glu | Gly | Val | Ile | Phe | Ala | Leu | Thr | Glu | Glu | Thr | Pro | Leu | Asp | Phe | Gln | Glu | Gly | Val | Ile | Phe | Ala | Leu | Thr |
| 260 | | | | | | | | | | 265 | | | | | | | | | | 270 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser | Ile | Val | His | Lys | Arg | Leu | Ile | Gln | Ala | Ile | Gln | Lys | Gly | Val | Lys | Ser | Ile | Val | His | Lys | Arg | Leu | Ile | Gln | Ala | Ile | Gln | Lys | Gly | Val | Lys | Ser | Ile | Val | His | Lys | Arg | Leu | Ile | Gln | Ala | Ile | Gln | Lys | Gly | Val | Lys |
| 275 | | | | | | | | | | 280 | | | | | | | | | | 285 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Gln | Phe | Ser | Phe | Arg | Pro | Phe | Gly | Tyr | Thr | Asn | Leu | Phe | Asp | Leu | His | Gln | Phe | Ser | Phe | Arg | Pro | Phe | Gly | Tyr | Thr | Asn | Leu | Phe | Asp | Leu | His | Gln | Phe | Ser | Phe | Arg | Pro | Phe | Gly | Tyr | Thr | Asn | Leu | Phe | Asp | Leu | His |
| 290 | | | | | | | | | | 295 | | | | | | | | | | 300 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Gln | Tyr | Gly | Tyr | Val | Gly | Ile | Gly | Met | Ser | Ala | Ala | Asn | Met | Ala | Tyr | Gln | Tyr | Gly | Tyr | Val | Gly | Ile | Gly | Met | Ser | Ala | Ala | Asn | Met | Ala | Tyr | Gln | Tyr | Gly | Tyr | Val | Gly | Ile | Gly | Met | Ser | Ala | Ala | Asn | Met | Ala | Tyr |
| 305 | | | | | | | | | | 310 | | | | | | | | | | 315 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu | Leu | Val | Val | His | Ser | Arg | Phe | Lys | Arg | Cys | Val | Phe | Ile | Gly | Gln | Glu | Leu | Val | Val | His | Ser | Arg | Phe | Lys | Arg | Cys | Val | Phe | Ile | Gly | Gln | Glu | Leu | Val | Val | His | Ser | Arg | Phe | Lys | Arg | Cys | Val | Phe | Ile | Gly | Gln |
| 325 | | | | | | | | | | 330 | | | | | | | | | | 335 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asp | Leu | Ser | Phe | Ser | Gln | Ser | Gly | Asn | Ser | His | Ala | Ser | Gly | Ala | Ile | Asp | Leu | Ser | Phe | Ser | Gln | Ser | Gly | Asn | Ser | His | Ala | Ser | Gly | Ala | Ile | Asp | Leu | Ser | Phe | Ser | Gln | Ser | Gly | Asn | Ser | His | Ala | Ser | Gly | Ala | Ile |
| 340 | | | | | | | | | | 345 | | | | | | | | | | 350 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Tyr | Gly | Asp | Arg | Glu | Ile | Lys | Pro | Lys | Lys | Asp | Lys | Asp | Lys | Ile | Phe | Tyr | Gly | Asp | Arg | Glu | Ile | Lys | Pro | Lys | Lys | Asp | Lys | Asp | Lys | Ile | Phe | Tyr | Gly | Asp | Arg | Glu | Ile | Lys | Pro | Lys | Lys | Asp | Lys | Asp | Lys | Ile | Phe |
| 355 | | | | | | | | | | 360 | | | | | | | | | | 365 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile | Glu | Lys | Tyr | Gly | Gly | Asn | Gly | Lys | Val | Glu | Thr | Thr | Leu | Val | Trp | Ile | Glu | Lys | Tyr | Gly | Gly | Asn | Gly | Lys | Val | Glu | Thr | Thr | Leu | Val | Trp | Ile | Glu | Lys | Tyr | Gly | Gly | Asn | Gly | Lys | Val | Glu | Thr | Thr | Leu | Val | Trp |
| 370 | | | | | | | | | | 375 | | | | | | | | | | 380 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Leu | Phe | Leu | Glu | Phe | Phe | Glu | Lys | Asp | Ile | Phe | Asn | Thr | Pro | Tyr | Lys | Leu | Phe | Leu | Glu | Phe | Phe | Glu | Lys | Asp | Ile | Phe | Asn | Thr | Pro | Tyr | Lys | Leu | Phe | Leu | Glu | Phe | Phe | Glu | Lys | Asp | Ile | Phe | Asn | Thr | Pro | Tyr |
| 385 | | | | | | | | | | 390 | | | | | | | | | | 395 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Leu | Glu | Val | Ile | Asn | Ala | Thr | Glu | Gly | Gly | Ala | Arg | Ile | Lys | Gly | Lys | Leu | Glu | Val | Ile | Asn | Ala | Thr | Glu | Gly | Gly | Ala | Arg | Ile | Lys | Gly | Lys | Leu | Glu | Val | Ile | Asn | Ala | Thr | Glu | Gly | Gly | Ala | Arg | Ile | Lys | Gly |
| 405 | | | | | | | | | | 410 | | | | | | | | | | 415 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Thr | Lys | Glu | Met | Pro | Phe | Lys | Glu | Val | Cys | Glu | Lys | Ile | Asp | Lys | Ser | Thr | Lys | Glu | Met | Pro | Phe | Lys | Glu | Val | Cys | Glu | Lys | Ile | Asp | Lys | Ser | Thr | Lys | Glu | Met | Pro | Phe | Lys | Glu | Val | Cys | Glu | Lys | Ile | Asp | Lys | Ser |
| 420 | | | | | | | | | | 425 | | | | | | | | | | 430 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys | Pro | Lys | Pro | Pro | Ile | Asn | Leu | Ile | Tyr | Pro | Thr | Gln | Ser | Glu | Gln | Lys | Pro | Lys | Pro | Pro | Ile | Asn | Leu | Ile | Tyr | Pro | Thr | Gln | Ser | Glu | Gln | Lys | Pro | Lys | Pro | Pro | Ile | Asn | Leu | Ile | Tyr | Pro | Thr | Gln | Ser | Glu | Gln |
| 435 | | | | | | | | | | 440 | | | | | | | | | | 445 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Lys | Asn | Leu | Lys | Ile | Ala | Lys | Lys | Lys | Cys | Glu | Glu | Ile | Ile | Lys | Ala | Lys | Asn | Leu | Lys | Ile | Ala | Lys | Lys | Lys | Cys | Glu | Glu | Ile | Ile | Lys | Ala | Lys | Asn | Leu | Lys | Ile | Ala | Lys | Lys | Lys | Cys | Glu | Glu | Ile | Ile | Lys |
| 450 | | | | | | | | | | 455 | | | | | | | | | | 460 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Tyr | Ala | Asn | Glu | Lys | Lys | Thr | Gln | Val | Glu | Glu | Ala | Phe | Leu | Lys | Val | Tyr | Ala | Asn | Glu | Lys | Lys | Thr | Gln | Val | Glu | Glu | Ala | Phe | Leu | Lys | Val | Tyr | Ala | Asn | Glu | Lys | Lys | Thr | Gln | Val | Glu | Glu | Ala | Phe | Leu | Lys | Val |
| 465 | | | | | | | | | | 470 | | | | | | | | | | 475 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala | Glu | Phe | Leu | Glu | Lys | Val | Glu | Lys | Leu | His | Glu | Lys | Asn | Lys | Leu | Ala | Glu | Phe | Leu | Glu | Lys | Val | Glu | Lys | Leu | His | Glu | Lys | Asn | Lys | Leu | Ala | Glu | Phe | Leu | Glu | Lys | Val | Glu | Lys | Leu | His | Glu | Lys | Asn | Lys | Leu |
| 485 | | | | | | | | | | 490 | | | | | | | | | | 495 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu | Glu | Leu | Asp | Phe | Glu | Glu | Leu | Glu | Asn | Leu | Ser | Ala | Glu | Ile | Asp | Glu | Glu | Leu | Asp | Phe | Glu | Glu | Leu | Glu | Asn | Leu | Ser | Ala | Glu | Ile | Asp | Glu | Glu | Leu | Asp | Phe | Glu | Glu | Leu | Glu | Asn | Leu | Ser | Ala | Glu | Ile | Asp |
| 500 | | | | | | | | | | 505 | | | | | | | | | | 510 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asn | Val | Lys | Glu | Leu | Phe | Asp | Asp | Lys | Arg | Phe | Asn | Ser | Tyr | Phe | Met | Asn | Val | Lys | Glu | Leu | Phe | Asp | Asp | Lys | Arg | Phe | Asn | Ser | Tyr | Phe | Met | Asn | Val | Lys | Glu | Leu | Phe | Asp | Asp | Lys | Arg | Phe | Asn | Ser | Tyr | Phe | Met |
| 515 | | | | | | | | | | 520 | | | | | | | | | | 525 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Asp | Ala | Ile | Gln | Ser | Tyr | Ile | Phe | His | Gln | Glu | Leu | His | Ile | Ala | Glu | Asp | Ala | Ile | Gln | Ser | Tyr | Ile | Phe | His | Gln | Glu | Leu | His | Ile | Ala | Glu | Asp | Ala | Ile | Gln | Ser | Tyr | Ile | Phe | His | Gln | Glu | Leu | His | Ile | Ala | Glu |
| 530 | | | | | | | | | | 535 | | | | | | | | | | 540 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile | Val | Cys | Lys | Lys | Thr | Ser | Asn | Glu | Asp | Gly | Leu | Arg | Ala | Lys | Gln | Ile | Val | Cys | Lys | Lys | Thr | Ser | Asn | Glu | Asp | Gly | Leu | Arg | Ala | Lys | Gln | Ile | Val | Cys | Lys | Lys | Thr | Ser | Asn | Glu | Asp | Gly | Leu | Arg | Ala | Lys | Gln |
| 545 | | | | | | | | | | 550 | | | | | | | | | | 555 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Leu | Glu | Tyr | Ile | Tyr | Ala | His | Lys | Tyr | Trp | Leu | Phe | Ser | Leu | Ala | Gly | Leu | Glu | Tyr | Ile | Tyr | Ala | His | Lys | Tyr | Trp | Leu | Phe | Ser | Leu | Ala | Gly | Leu | Glu | Tyr | Ile | Tyr | Ala | His | Lys | Tyr | Trp | Leu | Phe | Ser | Leu | Ala | Gly |
| 565 | | | | | | | | | | 570 | | | | | | | | | | 575 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Gly | Met | Asp | Cys | Val | Ile | Glu | Ala | Ile | Lys | Met | Ala | Leu | Lys | Glu | Trp | Gly | Met | Asp | Cys | Val | Ile | Glu | Ala | Ile | Lys | Met | Ala | Leu | Lys | Glu | Trp | Gly | Met | Asp | Cys | Val | Ile | Glu | Ala | Ile | Lys | Met | Ala | Leu | Lys | Glu | Trp |
| 580 | | | | | | | | | | 585 | | | | | | | | | | 590 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524

```

Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1           5           10           15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Pro Pro Thr Arg Ser Ile Gln
          20           25           30
Gly Leu Gln Asn Ile Gln Gln Asn Ile Pro Pro Gln Val Leu Thr Pro
          35           40           45
Gln Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
          50           55           60
Ser Ser Thr Leu Glu Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val
65           70           75           80
Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly Lys
          85           90           95
Ile His Asp Gly Ala His Cys Arg Ile Glu Cys Lys Lys Thr Pro Met
          100          105          110
Lys Cys Ile Ala
          115

```

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525

```

Arg Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val
1           5           10           15
Ser His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr
          20           25           30
Gly Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln
          35           40           45
Lys Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu
          50           55           60
Ala Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser
65           70           75           80
Pro Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr
          85           90           95
Gly Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln
          100          105          110
Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu Ile
          115          120          125
Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu Asn
          130          135          140
Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu

```

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```

145          150          155          160
Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro Ser
165          170          175
Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu
180          185          190
His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg
195          200          205
Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu Cys
210          215          220
Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu Trp
225          230          235          240
Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly Ser
245          250          255
Ala Leu Met Val Phe Leu Asn Ser Leu Ile Phe Met Leu Ala Ala Leu
260          265          270
Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr
275          280          285
Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly
290          295          300
Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val
305          310          315          320
Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn
325          330          335
His Met His Ala Glu Phe Ile Asp Val Tyr Ile His Phe Tyr Ala Leu
340          345          350
Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu Ser
355          360          365
Ser Leu Lys Lys Ala Cys Glu Asn Ala
370          375

```

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526

```

Thr Leu Lys Gly Ile Val Leu Phe Arg Leu Ile Ser Ala Trp Val Leu
1          5          10          15
Gln Asp Lys Phe Leu Phe Val Val Cys Phe Ile Leu Pro Phe Cys Leu
20          25          30
Gly Val Leu Gly Thr Gln Ile Phe Lys Gln Glu Thr Pro Arg Gln Leu
35          40          45
Pro Ile Val Val Val Asp Leu Asp Lys Thr Thr Thr Ser His Gln Val
50          55          60
Ala Phe Glu Leu Gly Ala Thr Ser Ala Val Glu Ile Lys Tyr Gln Val
65          70          75          80
Thr Ser Leu Ser Glu Ala Lys Arg Phe
85

```

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(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527

```

Ser Met Lys Lys Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser
1          5          10          15
Ser Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu
          20          25          30
Asn Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys
          35          40          45
Leu Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly
          50          55          60
Leu His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528

```

Val Arg Arg Gln Thr Met Lys Lys Val Ile Val Ala Leu Gly Val Leu
1          5          10          15
Ala Phe Ala Asn Val Leu Met Ala Thr Asp Val Lys Ala Leu Val Lys
          20          25          30
Gly Cys Ala Ala Cys His Gly Val Lys Phe Glu Lys Lys Ala Leu Gly
          35          40          45
Lys Ser Lys Ile Val Asn Met Met Ser Glu Lys Glu Ile Glu Glu Asp
          50          55          60
Leu Met Ala Phe Lys Ser Gly Ala Asn Lys Asn Pro Val Met Thr Ala
65          70          75          80
Gln Ala Lys Lys Leu Ser Asp Glu Asp Ile Lys Ala Leu Ala Ile Tyr
          85          90          95
Ile Pro Thr Leu Lys

```

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(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529

```

Arg Pro Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile
1      5      10      15
Met Ser Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg
20      25      30
Ile Asp Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu
35      40      45
Gly Glu Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile
50      55      60
Gly Thr Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg Trp Ile Ala
65      70      75      80
Tyr Asp Phe Pro Ser Asn Met Glu His Lys Phe Tyr Ser Phe Asp Gly
85      90      95
Gln Lys Gln Arg Tyr Phe Leu Val Arg Leu Lys His Val Asn Asn Ile
100     105     110
Asp Leu Asn Lys His Thr Pro Glu Phe Arg Ser Tyr Gln Phe Ile Gln
115     120     125
Leu Lys Asp Leu Leu Lys Lys Ile Val Pro Phe Lys Arg Gln Val Tyr
130     135     140
Arg Gln Val Ile Ala Tyr Phe Arg Lys Glu Gly Tyr Leu Gly Cys
145     150     155

```

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530

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Cys Met Asn Leu Val Phe Leu Trp Ala Ala Leu Gly Gly Ala Ile Gly
 1 5 10 15
 Ser Ser Leu Arg Tyr Phe Val Gly Lys Met Met Pro Ser Lys Phe Leu
 20 25 30
 Met Phe Glu Ser Phe Pro Leu Gly Thr Phe Ser Val Asn Leu Ile Gly
 35 40 45
 Cys Phe Ile Ile Gly Phe Met Gly His Leu Ala Ala Lys Lys Val Phe
 50 55 60
 Gly Asp Asp Phe Gly Ile Phe Phe Val Thr Gly Val Leu Gly Gly Phe
 65 70 75 80
 Thr Thr Phe Ser Ser Tyr Gly Leu Asp Thr Leu Lys Leu Leu Gln Lys
 85 90 95
 Ser Gln Tyr Leu Glu Ala Ile Ser Tyr Val Leu Gly Thr Asn Leu Leu
 100 105 110
 Gly Leu Ile Gly Val Ala Ile Gly Trp Phe Leu Ala Lys Asn Phe Val
 115 120 125
 Gly Val Asn
 130

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531

Tyr Leu Ser Ile Val Val Glu Asp Gln Lys Gly Ile Phe Pro Ile Ala
 1 5 10 15
 Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu Asp Val Cys
 20 25 30
 Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile Glu Gly Leu
 35 40 45
 Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe Gly His Ala
 50 55 60
 Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu Glu Asn Glu
 65 70 75 80
 Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met Phe Leu Met
 85 90 95
 Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly Thr Gly Arg
 100 105 110
 Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys Ala Tyr Lys
 115 120 125
 Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly Leu Leu Asn
 130 135 140
 Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr Lys Asn Leu
 145 150 155 160
 Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys Met Glu Cys
 165 170 175
 Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser Leu Thr Pro
 180 185 190
 Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu Lys Glu Arg

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```

      195      200      205
Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp Glu Leu Leu
  210      215      220
Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val Cys His Met
  225      230      235      240
Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Ser Ile Ala Leu
      245      250      255
Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Cys Phe Lys Asp
      260      265      270
Ser

```

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532

```

Arg Phe Leu Gln Lys Ser Ala Gln Ile Trp Gly Ile Lys Met Leu Val
 1      5      10      15
Glu Ile Glu Asn Leu Thr Lys Thr Tyr Gly Ser Leu Lys Ala Leu Asp
      20      25      30
Asn Ile Ser Leu Lys Leu Pro Lys Gln Gln Phe Ile Gly Leu Leu Gly
      35      40      45
Pro Asn Gly Ala Gly Lys Thr Thr Leu Leu Lys Ile Leu Ala Gly Leu
      50      55      60
Asn Leu Asn Tyr Gln Gly Glu Val Lys Ile Leu Asn Gln Lys Ile Gly
      65      70      75      80
Ile Glu Thr Lys Lys Ser Val Ala Phe Leu Ser Asp Gly Asp Phe Leu
      85      90      95
Asp Pro Lys Leu Thr Pro Leu Lys Ala Ile Ala Phe Tyr Lys Asp Phe
      100      105      110
Phe Ser Asp Phe Asp Glu Ser Lys Ala Leu Asn Leu Leu Lys Arg Phe
      115      120      125
Ser Val Pro Leu Lys Arg Glu Phe Lys Ala Leu Ser Lys Gly Met Arg
      130      135      140
Glu Lys Leu Gln Leu Ile Leu Thr Leu Ser Arg Asn Ala Ser Leu Tyr
      145      150      155      160
Leu Phe Asp Glu Pro Val Ala Gly Ile Asp Pro Ile Ala Arg Glu Glu
      165      170      175
Ile Phe Glu Leu Ile Ala Lys Glu Phe Ser Gln Asn Ala Ser Leu Leu
      180      185      190
Val Ser Thr His Leu Val Val Asp Val Glu Lys Tyr Leu Asp Ser Ala
      195      200      205
Ile Phe Leu Lys Glu Ala Lys Val Val Ala Phe Gly Asp Val Gly Glu
      210      215      220
Leu Lys Lys Gly Tyr Ser Ser Leu Glu Ala Ala Tyr Lys Glu Arg Leu
      225      230      235      240
Lys

```

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(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533

```

Lys Ser Trp Phe Phe Tyr Ala Pro Phe Tyr Gly Leu Trp Cys Leu Lys
1      5      10      15
Thr Pro Ile Ile Gly His Gly Met Lys Lys Lys Ala Lys Val Phe Trp
20      25      30
Cys Cys Phe Lys Met Ile Arg Trp Leu Tyr Leu Ala Val Phe Phe Leu
35      40      45
Leu Ser Val Ser Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys
50      55      60
Gln Asn His Lys Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys
65      70      75      80
Asp Asn Val Ile Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp
85      90      95
Val Tyr Ile Leu Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu
100      105      110
Ala Leu Leu Glu Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu
115      120      125
Val Lys Thr Asp Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile
130      135      140
Ile Phe Pro Phe Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser
145      150      155      160
Ala Asp Ile Ala Ser Gly Lys Asp Gln Lys Tyr Lys Ile Lys Asn Met
165      170      175
Ser Ala Ser Gly Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala
180      185      190
Thr Ser Gly Ser Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn
195      200      205
Pro Lys Ile Tyr Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile
210      215      220
Phe Met Ser Thr Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu
225      230      235      240
Phe Gly Thr Ser His Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr
245      250      255
Leu Ala Pro Lys Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg
260      265      270
Tyr Lys Arg Gly Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Pro
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534

```

Ile Val Arg Lys Lys Leu Met Leu Glu Met Ser Leu Gln Ala Leu Asn
1      5      10      15
Thr Gln Asp Ser Ser Val Met Ala Gln Ser Leu Leu Val His Ala Phe
20      25      30
Phe Ala Ala Leu Leu Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu
35      40      45
Phe Lys Glu Lys Asn Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val
50      55      60
Met Pro Ala Ile Tyr Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val
65      70      75      80
Phe Ile Trp Ala Met Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val
85      90      95
Met Leu Leu Gly Leu Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His
100      105      110
Lys Ser Val Lys Phe Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr
115      120      125
Ile Lys Lys Ala Lys Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile
130      135      140
Val Leu Met Gly Ile
145

```

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535

```

Pro Glu Gly Gly Asn Glu Leu Asn Val Phe Glu Pro Val Ile Ala Tyr
1      5      10      15
Lys Leu Phe His Ser Phe Val Ile Leu Gly Cys Ala Ile Glu Thr Leu
20      25      30
Thr Thr Lys Cys Val Glu Gly Ile Thr Ala Asn Glu Lys Ile Cys His
35      40      45
Asp Tyr Val Phe Asn Ser Ile Gly Ile Val Thr Ala Leu Asn Pro His
50      55      60

```

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Ile Gly Tyr Glu Lys Ser Ala Met Ile Ala Lys Glu Ala Leu Lys Ser
 65 70 75 80
 Asp Arg Ser Ile Tyr Asp Ile Ala Leu Glu Lys Lys Ile Leu Thr Lys
 85 90 95
 Glu Gln Leu Asp Asp Ile Phe Lys Pro Glu Asn Met Leu Ser Pro His
 100 105 110
 Ala Phe Lys Lys His Lys Asp
 115

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536

Lys Arg Leu Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn
 1 5 10 15
 Asp Phe Leu Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu
 20 25 30
 Leu Ser Leu Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser
 35 40 45
 Ile Val Asn Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr
 50 55 60
 Ala His Ser Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys
 65 70 75 80
 Ala Leu Val Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu
 85 90 95
 Val Ile Asn Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser
 100 105 110
 Tyr Leu His Gln Lys Tyr Tyr Pro His Val Val Leu Glu Glu Phe Gly
 115 120 125
 Ser Ile Leu Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met
 130 135 140
 Leu Leu Phe Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile
 145 150 155 160
 Gly Val Phe Gly Val Phe Phe Ser Ile Val Pro His Phe Leu Phe Phe
 165 170 175
 Lys Asn Thr Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln
 180 185 190
 Ser Tyr Gln Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe
 195 200 205
 Ser Phe Phe Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe
 210 215 220
 Ala Thr Leu Leu Gln Thr Leu Met Leu Thr His
 225 230 235

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537

```

Glu Cys Lys Gly Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu
1      5      10      15
Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val
20      25      30
Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn
35      40      45
Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro
50      55      60
Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp
65      70      75      80
His Ser Lys Tyr Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val
85      90      95
Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys
100     105     110
Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp
115     120     125
Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val
130     135     140
Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp
145     150     155     160
Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr
165     170     175
Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala
180     185     190
Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro
195     200     205
Tyr Ser Thr Asn Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe
210     215     220
Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val
225     230     235     240
Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala
245     250     255
Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly
260     265     270
Tyr Asn Tyr Thr Phe
275

```

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538

```

Ala Phe Glu Glu Leu Glu Pro Leu Ser Phe Ser Phe Asn Ser Pro Lys
1      5      10      15
Gly Ala Cys Glu Ser Cys Leu Gly Leu Gly Thr Lys Phe Ser Leu Asp
20      25      30
Ile Ser Lys Ile Leu Asp Pro Asn Thr Pro Leu Asn Gln Gly Ala Ile
35      40      45
Lys Val Ile Phe Gly Tyr Asn Arg Ser Tyr Tyr Ala Gln Met Phe Glu
50      55      60
Gly Phe Cys Thr Tyr Asn Gly Ile Asp Ser Ala Leu Cys Phe Asn Glu
65      70      75      80
Leu Asn Lys Glu Gln Gln Asp Ala Leu Leu Tyr Gly Asn Gly Thr Glu
85      90      95
Ile Ser Phe His Phe Lys Asn Ser Pro Leu Lys Arg Pro Trp Lys Gly
100      105      110
Ile Ile Gln Ile Ala Tyr Asp Met Phe Lys Glu Gln Lys Asp Leu Ser
115      120      125
Asp Tyr Met Ser Glu Lys Thr Cys Ser Ser Cys Asn Gly His Arg Leu
130      135      140
Lys Ala Ser Ser Leu Ser Val Gln Val Ala Gly Leu Lys Met Ala Asp
145      150      155      160
Phe Leu Thr Lys Pro Ile Glu Glu Val Tyr His Phe Phe Asn Asp Pro
165      170      175
Thr His Phe Asn Tyr Leu Asn Glu Gln Glu Lys Lys Ile Ala Glu Pro
180      185      190
Ile Leu Lys Glu Ile Leu Glu Arg Val Phe Phe Leu Tyr Asp Val Gly
195      200      205
Leu Gly Tyr Leu Thr Leu Gly Arg Asp Ala Arg Thr Ile Ser Gly Gly
210      215      220
Glu Ser Gln Arg Ile Arg Ile Ala Ser Gln Ile Gly Ser Gly Leu Thr
225      230      235      240
Gly Val Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Glu Lys
245      250      255
Asp Thr Leu Lys Leu Ile Asn Thr Leu Arg Asn Leu Gln Lys Lys Gly
260      265      270
Asn Thr Leu Ile Val Val Glu His Asp Lys Glu Thr Ile Lys His Ala
275      280      285
Asp Phe Val Val Asp Ile Gly Pro Lys Ala Gly Arg His Gly Gly Glu
290      295      300
Val Val Phe Ser Gly Ser Val Lys Asp Leu Leu Gln Asn Asn His Ser
305      310      315      320
Thr Ala Leu Tyr Leu Asn Gly Thr Lys Lys Ile Glu Arg Pro Lys Phe
325      330      335
Glu Pro Pro Lys Glu Lys His Phe Leu Glu Ile Lys Asn Val Asn Ile
340      345      350
Asn Asn Ile Lys Asn Leu Ser Val Gln Ile Pro Leu Lys Gln Leu Val
355      360      365
Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Ile Leu Gln
370      375      380
Thr Leu Leu Pro Thr Ala Gln Thr Leu Leu Asn His Ala Lys Lys Asn
385      390      395      400
Gln Ser Leu Asn Gly Val Glu Ile Val Gly Leu Glu Tyr Leu Asp Lys
405      410      415
Val Ile Tyr Leu Asp Gln Ala Pro Ile Gly Lys Thr Pro Arg Ser Asn
420      425      430
Pro Ala Thr Tyr Thr Gly Val Met Asp Glu Ile Arg Ile Leu Phe Ala

```

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```

      435              440              445
Glu Gln Lys Glu Ala Lys Ile Leu Gly Tyr Ser Thr Ser Arg Phe Ser
 450              455              460
Phe Asn Val Lys Gly Gly Arg Cys Glu Lys Cys Gln Gly Asp Gly Asp
 465              470              475              480
Ile Lys Ile Glu Met His Phe Leu Pro Asp Val Leu Val Gln Cys Asp
      485              490              495
Ser Cys Lys Gly Ala Lys Tyr Asn Pro Gln Thr Leu Glu Ile Lys Val
      500              505              510
Lys Gly Lys Ser Ile Ala Asp Val Leu Asn Met Ser Val Glu Glu Ala
      515              520              525
Tyr Glu Phe Phe Ala Lys Phe Pro Lys Ile Ala Val Lys Leu Lys Thr
 530              535              540
Leu Ile Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Asn Ala Thr
 545              550              555              560
Thr Leu Ser Gly Gly Glu Ala Gln Arg Ile Lys Leu Ala Lys Glu Leu
      565              570              575
Ser Lys Lys Asp Thr Gly Lys Thr Leu Tyr Ile Leu Asp Glu Pro Thr
      580              585              590
Thr Gly Leu His Phe Glu Asp Val Asn His Leu Leu Gln Val Leu His
      595              600              605
Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile Glu His Asn Leu
 610              615              620
Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met Gly Pro Asp Gly
 625              630              635              640
Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr Pro Leu Glu Val
      645              650              655
Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly Lys Phe Leu Ala
      660              665              670
Leu Glu Leu Lys
 675

```

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539

```

Ala Arg Phe Val Lys Ile Thr Ala Asp Tyr Phe Ser Pro Met Glu Asn
 1              5              10              15
Val Phe Tyr Arg Ser Ile Thr Met Thr Leu Leu Leu Leu Ile Tyr
      20              25              30
Pro Phe Lys Pro Tyr Arg Leu Lys Ser Tyr Lys Gln Gly Gly Phe Lys
      35              40              45
Lys Leu Ala Phe Arg Val Val Gly Gly Leu Ala Met Leu Ala Phe
 50              55              60
Phe Tyr Asn Ile Glu Lys Ile Ser Leu Ala Thr Ala Asn Ala Phe Ser
 65              70              75              80
Gln Cys Ala Pro Ile Tyr Thr Val Leu Leu Ser Pro Leu Leu Leu Lys
      85              90              95

```

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Glu Lys Leu Lys Arg Ser Ala Leu Ile Ser Ala Cys Ile Gly Leu Val
 100 105 110
 Gly Val Val Leu Ile Ser Asp Pro Ser Val Glu Asn Val Gly Leu Val
 115 120 125
 Glu Ile Ile Met Gly Ile Leu Ser Gly Ile Phe Val Ser Leu Ala Tyr
 130 135 140
 Ile Thr Leu Arg Asp Leu Arg Glu Tyr Tyr Asp Lys Gln Ala Val Ile
 145 150 155 160
 Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly Met Phe
 165 170 175
 Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg Lys Glu
 180 185 190
 Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu Gly Gln
 195 200 205
 Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile Ile Ala
 210 215 220
 Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly Leu Tyr
 225 230 235 240
 Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val Ala Leu
 245 250 255
 Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu Lys Glu
 260 265 270
 Leu Lys Lys Ile
 275

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540

Val Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr
 1 5 10 15
 Phe Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu
 20 25 30
 Ile Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met
 35 40 45
 Ser Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr
 50 55 60
 Ser Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu
 65 70 75 80
 Gly Gln Asn Asp Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val
 85 90 95
 Ile Asn Met Phe Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys
 100 105 110
 Pro Lys Asp Ala Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly
 115 120 125
 Val Asn Leu Phe Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser
 130 135 140
 Leu Gly Leu Leu Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro

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```

145      150      155      160
Tyr Leu Thr Leu Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro
      165      170      175
Leu Leu Leu Gly Val Phe Ala Tyr Ala Leu Arg Lys Arg Tyr Phe Lys
      180      185      190
Ser Ala Ile Phe Ala Leu Val Val Leu Ile Val Asn Thr Ala Leu Phe
      195      200      205
Ser Gly Asp Phe Asn Lys Gly Leu Pro Ser Gly Tyr Phe Ile Asp Thr
      210      215      220
Cys Leu Glu Leu Met Leu Leu Tyr Ser Pro Leu Leu Phe Leu Tyr Tyr
      225      230      235
Pro Tyr Thr Leu Tyr Lys Ala Leu Leu Asp Lys Lys Pro Ser Leu Leu
      245      250      255
Ala Phe Met Ala Arg Ala Ala Gly Phe Ser Leu Cys Phe
      260      265

```

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541

```

Ser Pro Phe Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn
1      5      10      15
Ala Tyr Ser Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg
      20      25      30
Pro Phe Ile Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys
      35      40      45
Gly Val Leu Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val
      50      55      60
His Leu Val Glu Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn
      65      70      75      80
Ala Leu Lys Phe Pro Asn Ala Gln Val Phe Glu Ser Asp Phe Leu Asp
      85      90      95
Phe Asn Pro Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Pro Phe
      100      105      110
Tyr Ala Leu Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His
      115      120      125
Gln Ser Glu Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Lys Cys
      130      135      140
Leu Lys Pro Lys Gly Tyr Phe Ile Phe Cys Tyr Glu Ala Leu Ser Leu
      145      150      155      160
Cys Leu Val Ile Glu Ser Leu Lys Ser Val Lys Leu Thr Leu Glu Thr
      165      170      175
Leu Arg Phe Val Gln Ser Phe Lys Asp Lys Asn Ala His Leu Met Leu
      180      185      190
Gly Ala Ala Arg Asn Asn Ser Lys Ser Ala Leu Lys Val Leu Pro Pro
      195      200      205
Leu Ile Thr His Asn Ser Lys Asn Gln Ser Asp Asn Thr Lys Glu Val
      210      215      220

```

SUBSTITUTE SHEET (RULE 26)

1099

Leu Asn Ile Tyr Gln Ile Cys Asn Thr Tyr Ser Ile Lys Ala Pro Leu
 225 230 235 240
 Asp

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542

Ser Arg Ser Phe Arg Gly Leu Leu Tyr Tyr Asn Lys Ile Asn Leu Ile
 1 5 10 15
 Asn Lys Asp Thr Gly Leu Gln Glu Ile Lys Leu Asp Ile Tyr Ala Thr
 20 25 30
 Leu Val Cys Met Val Leu Val Leu Leu Gly Arg Tyr Val Ile Ser
 35 40 45
 Lys Val Lys Phe Leu Arg Asp Tyr Asp Ile Pro Glu Pro Val Val Gly
 50 55 60
 Gly Val Leu Val Ala Phe Phe Ile Met Leu Ala Arg Gln Phe Tyr His
 65 70 75 80
 Phe Gly Leu Gln Phe Asp Ser Ser Leu Lys Asp Pro Leu Met Leu Thr
 85 90 95
 Phe Phe Ile Thr Ile Gly Leu Ser Ala Asp Phe Lys Ser Leu Gln Lys
 100 105 110
 Gly Gly Lys Met Leu Ala Val Phe Leu Leu Ala Val Ala Gly Phe Val
 115 120 125
 Val Cys Gln Asn Ala Val Gly Ile Ser Ile Ala Ser Leu Leu Gly Val
 130 135 140
 Asn Pro Leu Met Gly Leu Leu Gly Gly Ser Ile Ala Leu Val Gly Gly
 145 150 155 160
 His Gly Thr Ser Ala Ala Trp Ala Asn Phe Phe Thr Gln Pro Pro Tyr
 165 170 175
 His Phe Ser Ser Ser Leu Glu Val Gly Met Ala Cys Ala Thr Phe Gly
 180 185 190
 Leu Val Ser Gly Gly Ile Ile Gly Gly Pro Val Ala Lys Tyr Leu Ile
 195 200 205
 Ser Lys Tyr Lys Leu Glu Pro Lys Asp Thr Lys Glu Lys Asp Thr Leu
 210 215 220
 Glu Gly Val Val Ser Lys Gly Phe Glu Thr Pro Lys Glu Gln Arg Leu
 225 230 235 240
 Ile Thr Ala Ser Ser Phe Val Glu Thr Leu Ala Leu Ile Ala Ile Ala
 245 250 255
 Leu Leu Val Gly Thr Phe Leu Ser His Leu Met Pro Lys Ser Phe Thr
 260 265 270
 Leu Pro Thr Phe Val Trp Cys Leu Phe Val Gly Val Ile Leu Arg Asn
 275 280 285
 Ala Leu Ser Phe Phe Lys Ile His Ser Val Phe Asp Arg Glu Val Ser
 290 295 300
 Val Ile Gly Asn Val Ser Leu Ser Leu Phe Leu Ala Tyr Ala Leu Met

SUBSTITUTE SHEET (RULE 26)

1100

```

305          310          315          320
Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala Val
          325          330          335
Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu Val
          340          345          350
Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys Ala
          355          360          365
Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val Asn
          370          375          380
Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe Ile
385          390          395          400
Val Val Pro Leu Val Gly Ala Phe Phe Val Asp Ile Ile Asn Ala Leu
          405          410          415
Ala Ile Lys Gly Phe Leu Leu Leu Pro Phe Phe Pro Ser
          420          425

```

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543

```

Lys Phe Val Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr
1          5          10          15
Glu Lys Gly Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu
          20          25          30
Ser Glu Asp Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala
          35          40          45
Val Leu Gln Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly
          50          55          60
Ser Gly Asp Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val
65          70          75          80
Gly Arg Phe Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro
          85          90          95
Met Cys Gln Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile
          100          105          110
Lys Ala Trp Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val
          115          120          125
Asp Cys Val Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu
130          135          140
Asp Phe Glu Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp
145          150          155          160
Ile Pro Ser Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Arg Leu
          165          170          175
Arg Arg Ile Arg Leu Ser Ala Trp Ala Leu Ser Ser His Ala Tyr
          180          185          190

```

(2) INFORMATION FOR SEQ ID NO:1544:

SUBSTITUTE SHEET (RULE 26)

1101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544

```

Asn Ala His Asn Leu Lys Asp Lys Thr Phe Gln Gly Gly Phe Glu Leu
1      5      10      15
Leu Thr Thr Pro Lys Glu Tyr Ser Trp Cys Gly Val Val Leu Ser Leu
      20      25      30
Leu Leu Ala Ile Asn Leu Tyr Leu Glu Tyr Leu Asn His Gln Lys Leu
      35      40      45
Asp Phe Ser Lys Pro Thr Ser Leu Asn Ala Gln Ile Leu Leu Gln Tyr
      50      55      60
Pro Lys Thr Lys Asp Gln Lys Thr Tyr Phe Val Leu Lys Leu Gln Ser
      65      70      75      80
Lys Gly Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu
      85      90      95
Gln Tyr Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe
      100      105      110
Leu Glu Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu
      115      120      125
Thr Arg Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser
      130      135      140
Ala His Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile
      145      150      155      160
Gly Asp Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly
      165      170      175
Ile Asn His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser
      180      185      190
Ala Ser Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys
      195      200      205
Arg Tyr Phe Pro Tyr Arg Asn Ala Phe Tyr Asp Ile Gly Val Leu Val
      210      215      220
Trp Val Phe Leu Leu Gly Tyr Leu Leu Leu Asp Phe Leu Pro Ser
      225      230      235      240
Phe Phe Arg Ala Phe Leu Met Gly Leu Leu Gly Phe Leu Ala Cys Phe
      245      250      255
Phe Gly Val Arg Ile Leu Ser Phe Lys Leu Leu Val Leu Ala Cys Cys
      260      265      270
Ile Ala Ile Ala Leu Leu Pro Lys Leu Leu Phe Ser Val Gly Phe Leu
      275      280      285
Leu Ser Val Cys Gly Val Trp Tyr Ile Phe Leu Phe Leu Lys His Thr
      290      295      300
Gln Ile Phe Phe Lys Asp Ser Ser Phe Phe Lys Arg Ser Phe Gln Ala
      305      310      315      320
Ile Ala Leu Ser Val Leu Val Phe Leu Asn Met Leu Ile Val Ala His
      325      330      335
Ala Phe Phe Pro Met Phe Ser Pro Tyr Gln Leu Phe Ser Ile Pro Leu
      340      345      350
Gly Leu Ile Phe Thr Val Phe Phe Pro Leu Ser Leu Phe Leu His Ala
      355      360      365
Val Gly Leu Gly Ser Leu Leu Asp Asn Ile Leu Ser Met Pro Leu Thr

```

SUBSTITUTE SHEET (RULE 26)

1102

```

      370              375              380
Ile Pro Thr Ile Ser Val Ser Ser Pro Leu Trp Leu Leu Gly Ala His
385              390              395              400
Leu Phe Leu Thr Ile Leu Ser Val Arg Phe Phe Lys Val Tyr Leu Ser
      405              410              415
Met Asn Val Leu Ser Met Gly Phe Phe Leu Tyr Cys Cys Tyr Gln Tyr
      420              425              430
Ile Ile Met Pro Ser Leu Ile Val Gly
      435              440

```

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545

```

Glu Ala Phe Lys Ala Asp Thr Thr Ile Ser Met Gly Ala Ile Lys Ser
1              5              10              15
Cys Leu Leu Ser Asp Lys Ala Lys Asp Tyr Ile Gly Glu Leu Lys Val
      20              25              30
Gly His Leu Gly Val Phe Asn Gln Ile Tyr Glu Ile Pro Thr Asp Thr
      35              40              45
Phe Leu Leu Glu Lys Ser Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys
      50              55              60
Asn Ala His Lys Gly Asp Tyr Gly His Ala His Val Leu Leu Gly Lys
      65              70              75              80
His Ser Gly Ala Gly Leu Leu Ser Ala Leu Ser Ala Leu Ser Phe Gly
      85              90              95
Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys Glu Ile Thr Ser Asn
      100              105              110
Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn Phe Pro Lys Lys Leu
      115              120              125
Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn Ile Pro Lys Asp Phe
      130              135              140
Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu Asp Ala Gly Val Phe
      145              150              155              160
Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys Glu Val Ile Leu Thr
      165              170              175
Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys Ser Val Gly Ile Asn
      180              185              190
Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu Glu Ile Ala Arg Asp
      195              200              205
Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu Leu Lys Gly Ala Asn
      210              215              220
Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile Asn Asn Leu Gly Ser
      225              230              235              240
Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val Leu Ala Gly Leu Ile
      245              250              255
Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu Asp Ala Ala Ile Asn
      260              265              270

```

SUBSTITUTE SHEET (RULE 26)

1103

Ala Ser Leu Ala His Ala Leu Ala Gly Leu Glu Phe Lys Asn His Tyr
 275 280 285
 Ala Leu Thr Pro Leu Asp Leu Ile Glu Lys Ile Lys Arg Leu
 290 295 300

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546

Leu Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Val Ala
 1 5 10 15
 Thr Met Leu Ala Val Gly Phe Ser Leu Asp Glu Ile Lys Asn Asp Ile
 20 25 30
 Thr Asn Thr Pro Ala Ser Phe Glu Pro Ser Leu Asp Tyr Ile Val Val
 35 40 45
 Lys Ile Pro Arg Phe Ala Phe Glu Lys Phe Ala Gly Val Ser Ser Thr
 50 55 60
 Leu Gly Thr Ser Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly
 65 70 75 80
 Asn Phe Leu Glu Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn
 85 90 95
 Trp Leu Gly Phe Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys
 100 105 110
 Glu Ile Arg Arg Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala
 115 120 125
 Phe Arg Leu Gly Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile
 130 135 140
 Asp Arg Trp Phe Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu
 145 150 155 160
 Gly Ile Asn Ser Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu
 165 170 175
 Lys Asn Leu Gly Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu
 180 185 190
 Asn Glu Asn Leu Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser
 195 200 205
 Asn Leu Gln Ile Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala
 210 215 220
 Glu Phe Leu Ser Leu Thr Pro Tyr Leu Tyr Ser Thr Tyr Ala Pro Asn
 225 230 235 240
 Pro Leu Pro Pro Ile Gly Asn Lys Gln Glu Lys Gln Glu Lys Lys Ile
 245 250 255
 Leu Ile Ile Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe
 260 265 270
 Asp Tyr Cys Cys Val His Ala Ser Phe Ala Leu Lys Asp Leu Asn Ile
 275 280 285
 Lys Ser Val Met Leu Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr
 290 295 300
 Asp Thr Ser Asp Thr Leu Tyr Phe Glu Pro Ile His Phe Glu Cys Val

SUBSTITUTE SHEET (RULE 26)

1104

```

305          310          315          320
Lys Ser Ile Ile Gln Arg Glu Arg Val Asp Gly Ile Ile Val His Phe
          325          330          335
Gly Gly Gln Thr Pro Leu Lys Leu Ala Lys Asp Leu Ala Lys Met Gln
          340          345          350
Ala Pro Ile Ile Gly Thr Pro Phe Lys Val Ile Asp Ile Ala Glu Asp
          355          360          365
Arg Glu Lys Phe Pro Ser Phe
          370          375

```

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547

```

Arg Pro Val Ile Ser Ala Lys Glu Gly Ser Asp Pro Ser Ser Leu Ala
1          5          10          15
Tyr Asn Thr Ile Glu Ser Ala Ile Ala Lys Asn Ile Asp Glu Val Phe
          20          25          30
Ile Asp Thr Ala Gly Arg Leu His Asn Gln Thr Asn Leu Lys Asn Glu
          35          40          45
Leu Ser Lys Ile Ala His Thr Cys Ser Lys Val Leu Lys Asp Ala Pro
          50          55          60
Phe Tyr Lys Phe Leu Ile Leu Asp Gly Thr Gln Gly Ser Ser Gly Leu
          65          70          75          80
Thr Gln Ala Lys Ile Phe His Glu Thr Leu Ala Leu Asp Gly Val Ile
          85          90          95
Met Thr Lys Leu Asp Gly Thr Ser Lys Gly Gly Ala Ile Leu Ser Val
          100          105          110
Leu Tyr Glu Leu Lys Leu Pro Ile Leu Tyr Leu Gly Met Gly Glu Lys
          115          120          125
Glu Asp Asp Leu Ile Ala Phe Asp Glu Glu Arg Phe Ile Glu Asp Leu
          130          135          140
Val Asp Ala Val Phe Val Glu Gln
          145          150

```

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

1105

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548

```

Asn Leu Arg Ile Ile Thr Ile Lys Thr Ile Phe Arg Asp Phe Cys Lys
1           5           10           15
Glu Arg Leu Lys Arg Ala Lys Ser Lys Asn Lys Val Arg Asp Lys Leu
          20           25           30
Ala Cys Lys Leu Leu Phe Trp Lys Leu Lys Asp Tyr Gln Asn Ile Leu
          35           40           45
Leu Tyr Ser Pro Leu Gly His Glu Leu Asp Ile Arg Pro Leu Ile Leu
          50           55           60
Lys Leu Arg Gln Lys Asn Lys Arg Val Trp Leu Pro Lys Ser Ile Lys
          65           70           75           80
Lys Gly Ala His Phe Ser Lys Glu Gly Phe Thr Ile Ala Pro Phe Arg
          85           90           95
Leu Pro Leu Arg Arg Leu Gly Trp Phe Asp Glu Pro Ser Leu Ser Arg
          100          105          110
Tyr Tyr Lys Arg Glu Leu Asp Cys Ile Val Val Pro Ile Leu Gly Met
          115          120          125
Asp Thr Ser Phe Arg Arg Val Gly Phe Gly Leu Gly Met Tyr Asp Arg
          130          135          140
Ser Leu Pro Gln Leu Phe Lys Lys Gln Leu Lys Arg Pro Leu Val Ile
          145          150          155          160
Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu Thr Asp Ala
          165          170          175
Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile Val Met Lys
          180          185          190
Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu His Phe Ile
          195          200          205
Arg Ser Leu Gly Ser Val Phe Asp His Arg Ser Asn His Val Leu Cys
          210          215          220
Asp Glu Lys Asp Leu Leu Arg
225          230

```

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549

```

Arg Ile Ile Lys Gly Asn Ile Met Ser Ser Gly Leu Ile Tyr Ile Ser
1           5           10           15
Leu Glu Val Leu Val Ala Cys Leu Ile Thr Ala Leu Ile Met Tyr Tyr
          20           25           30
Val Met Lys Lys Ile Tyr Tyr Ala Arg Gly Gln Ala Ile Leu Lys Gly

```

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1106

```

      35          40          45
Ala Ser Ala Lys Ala Lys Leu Met Glu Phe Gln Ala Lys Ser Phe Val
  50          55          60
Glu Ala Glu Glu Met Arg Met Lys Ser Gln Glu Cys Lys Leu Gln Gln
  65          70          75          80
Gln Tyr Glu Asn Lys Asn Leu Gln Leu Gln Thr His Phe Asp Lys Lys
      85          90          95
Glu Ala His Leu Lys His Leu Glu Ala Gln His Lys Glu Phe Val Arg
      100          105          110
Asp Glu Lys Arg Tyr Leu Glu Lys Glu Lys Lys Glu Leu Glu Lys Glu
      115          120          125
Arg Gln Ile Leu Glu Gln Glu Arg Glu Asn Phe Lys Lys Gln Arg Ala
      130          135          140
Ile Cys Lys Glu Ala Gln Ala Lys Ala Leu Asp Ala Met Leu Asn Tyr
      145          150          155          160
Met Ala Tyr Thr Lys Asp Glu Ile Lys Ser Met Ile Leu Glu Gln Leu
      165          170          175
Glu Gln Glu Leu Glu Ala Gln Lys Ser Ala Leu Ile Arg Arg Tyr Glu
      180          185          190
Glu Glu Ala Phe Ile Met Cys Leu
      195          200

```

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550

```

Ile Arg Ser Ser Asn Asp Thr Gln Thr Thr Gln Thr Pro Trp His Ser
  1          5          10          15
Asn Thr Arg Arg Pro Lys Pro Thr Pro Lys Pro Ile Lys Lys Glu Ala
      20          25          30
Lys Lys Ala Lys Glu Lys Thr Thr Lys His Ala His Ser Lys His Ala
      35          40          45
His Ser Pro Leu Asn Glu Arg Ser Ala Lys Lys Glu Ile Pro Lys Lys
      50          55          60
Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu
      65          70          75          80
Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ile
      85          90          95
Pro Lys Lys Glu Ala Glu Asn Glu Ser Lys Asn Gln Ile Phe Ile Ala
      100          105          110
Glu Lys Asn Asp Thr Trp Ile Lys Thr Lys Arg Lys Lys His Lys Lys
      115          120          125
Ile Val Leu Asp Ala Gly His Gly Gly Lys Asp Cys Gly Ala Met Ser
      130          135          140
Ala Asn Leu Val Cys Glu Lys Asp Ile Val Leu Glu Val Val Lys Phe
      145          150          155          160
Leu His Lys Glu Leu Lys Lys Arg Gly Tyr Ser Val Leu Leu Thr Arg
      165          170          175

```

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Asp Lys Asp Ile Tyr Ile Asp Leu Val Ala Arg Thr Glu Leu Ala Asn
 180 185 190
 Lys Lys Gly Ala Asp Leu Phe Ile Ser Val His Ala Asn Ser Ile Pro
 195 200 205
 Lys Arg Ser Thr Ser Asn Ala His Gly Ile Glu Thr Tyr Phe Leu Ser
 210 215 220
 Thr Ala Arg Ser Glu Arg Ala Arg Lys Val Ala Glu Gln Glu Asn Lys
 225 230 235 240
 Asp Asp Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn
 245 250 255
 Ser Leu Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp
 260 265 270
 Val Gln Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val
 275 280 285
 Val Asp Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala
 290 295 300
 Leu Met Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile
 305 310 315 320
 Glu Ser Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys
 325 330 335
 Gly Ile Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
 340 345 350

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551

Arg Val Ser Met Asn Val Lys Lys Lys Gly Lys Pro Gln Ser Gly Lys
 1 5 10 15
 Ile Asp Arg Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr
 20 25 30
 Phe Leu Ser Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro
 35 40 45
 Ile Pro Gly Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met
 50 55 60
 Ser Lys Thr Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys
 65 70 75 80
 Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser
 85 90 95
 Ile Arg Gln Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu
 100 105 110
 Arg Tyr Phe His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu
 115 120 125
 Leu Glu Arg Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val
 130 135 140
 Asn Asn Lys Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn
 145 150 155 160
 Lys Gln Glu Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly Trp Asn

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1108

165 170 175
 Phe Val Thr Ser Arg Gly Lys Thr Glu Ile
 180 185

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552

Lys Arg Asp Gln Met Ala Glu Glu Glu Lys Thr Glu Leu Pro Ser Ala
 1 5 10 15
 Lys Lys Ile Gln Lys Ala Arg Glu Glu Gly Asn Val Pro Lys Ser Met
 20 25 30
 Glu Val Val Gly Phe Leu Gly Leu Leu Ala Gly Leu Met Ser Ile Phe
 35 40 45
 Val Phe Phe Ile Trp Trp Val Asp Gly Phe Ser Glu Met Tyr Arg His
 50 55 60
 Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu Ser Val Gln Glu
 65 70 75 80
 Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu Leu Leu Pro Val
 85 90 95
 Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn Val Leu Gln Phe
 100 105 110
 Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys Phe Ser Lys Ile
 115 120 125
 Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu Lys Lys Ile Leu
 130 135 140
 Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala Phe Phe Leu Gly
 145 150 155 160
 Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn His Ala Ala Leu
 165 170 175
 Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser Lys Ala Leu Trp
 180 185 190
 Leu Ile Ser Ser Leu Leu Phe Leu Phe Phe Val Leu Ala Phe Val Asp
 195 200 205
 Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu Lys Met Thr Lys
 210 215 220
 Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly Asn Pro Glu Ile
 225 230 235 240
 Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala Thr Asn Lys Met
 245 250 255
 Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr Asn Pro Thr His
 260 265 270
 Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro Val Pro Val Val
 275 280 285
 Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile Lys Gly Ile Ala
 290 295 300
 Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr Leu Ala Arg Glu
 305 310 315 320

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Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro Glu Glu Leu Phe
 325 330 335
 Glu Ala Val Ala Ile Val Phe Ala Gln Val Ala Lys Leu Glu Gln Glu
 340 345 350
 Arg Gln Lys Gln Lys Ile Ile Lys Pro Leu
 355 360

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553

Glu Asn Thr Met Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu
 1 5 10 15
 Ile Leu Ser Lys Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr
 20 25 30
 Lys Glu Asn Leu Lys Leu Ile Ser Phe Ile Thr Pro Lys Ile Ser Asn
 35 40 45
 Leu Glu Ile Tyr Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Ile
 50 55 60
 Lys Gly Ser Glu Trp Val Phe Asn Glu Asn Ser Leu Thr Asp Leu Ile
 65 70 75 80
 Asn Glu Gln Lys Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu
 85 90 95
 Ser Lys Met Ser Leu Gly Ala Val Val Arg Leu Ile Phe Cys Tyr Lys
 100 105 110
 Leu Glu Gly Val Ile Leu Asp Leu Arg Ala Tyr Arg Leu Arg Ala Tyr
 115 120 125
 Tyr His Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu
 130 135 140
 Leu Tyr Asn Tyr Ile Lys Ala His Ile Ala Leu Asn Leu Leu Trp Thr
 145 150 155 160
 Ile Arg Asn Arg Thr Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro
 165 170 175
 Asn Asn Arg Pro Gln
 180

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554

```

Ala Asn Gly Cys Glu Lys Arg Ile Phe Met Leu Leu Cys Ala Gly Arg
 1           5           10           15
Asn Glu Thr Leu Lys Lys Ala Val Pro Ile Gly Val Gly Leu Ile Glu
 20           25           30
Ser Ala Ile Asn Leu Thr Arg Met Cys Leu Lys Asn Pro Asp Thr Glu
 35           40           45
Ser Leu Ile Phe Ile Gly Ser Ala Gly Ser Tyr Ser Pro Glu Thr Glu
 50           55           60
Ile Leu Ser Val Phe Glu Ser Ile Glu Gly Tyr Gln Ile Glu Glu Ser
 65           70           75           80
Phe Ser His Leu Asn Ser Tyr Thr Pro Leu Asp Asn Phe Ile His Ile
 85           90           95
Glu Thr Lys Glu Gln Ala Leu Phe Glu Arg Val Arg Val Asn Ser Ser
100           105           110
Asn Tyr Ile His Thr Ser Glu Met Phe Ala Lys Lys Met Val Gln Lys
115           120           125
Gly Val Leu Leu Glu Asn Met Glu Phe Phe Ser Val Leu Ser Val Ala
130           135           140
Lys Ile Phe Ser Leu Lys Ala Lys Gly Ile Phe Cys Val Ser Asn His
145           150           155           160
Val Gly Leu Asn Ala His Lys Glu Phe Lys Glu Asn His Ala Lys Val
165           170           175
Lys Gln Ile Leu Glu Asn Ile Ile Asp Ser Leu Ile Val
180           185

```

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555

```

Phe Val Leu Ala Cys Asn Arg Leu Leu Ala Arg Thr Leu Lys Ser Glu
 1           5           10           15
Tyr Arg Ile Cys Gly Phe Ala Lys Asn His Pro Phe Ser Gly Pro Phe
 20           25           30
Glu Ser Gly Gly Val Trp Phe Cys Gly Tyr Ser Thr Phe Arg Leu Asn
 35           40           45
Arg Phe Ser Gly His Tyr Cys Lys Trp Arg Arg Asn Gly Ile Gln
 50           55           60
Ser Val Val Asp Glu Thr Lys Pro Phe Thr His Ser Lys Asn Gly Arg
 65           70           75           80

```

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Lys Arg Gly Phe Ser Leu Phe Gln Ala Ile Gln Pro Ser Val Phe Asp
 85 90 95
 Arg Ser Thr Leu Ala Asn Gln Ser Asp His Arg Tyr Phe His Leu Phe
 100 105 110
 Val Gly Tyr Phe Phe Glu Trp Val Pro Lys Asn Arg Phe Lys Glu Ser
 115 120 125
 Val Gln Cys Leu Arg Gly Gly Asp Leu Tyr Cys Asn His Gln His Ala
 130 135 140
 Gln Tyr Phe Lys Leu Glu Phe Asn Phe Arg Lys Lys Arg Ala Gly Tyr
 145 150 155 160
 Lys Arg Arg Tyr Asn Phe His Ala Val Phe Phe Gly Gly His Cys Arg
 165 170 175
 His Ala Arg Glu Thr Phe Phe Arg Gln Ser Ile Lys Leu Leu Arg Leu
 180 185 190
 Leu Arg Phe Ser Glu Lys Arg Lys Thr Lys Arg Ser Lys Asp Lys Glu
 195 200 205
 Arg Arg Lys Asp Cys Arg Lys Thr Arg Asn Gln Ala Arg Ser His Arg
 210 215 220
 Ala Lys Ser Gln Ser Arg His Arg Lys Arg Ser His Phe Arg Arg Glu
 225 230 235 240
 Lys Leu Pro Lys Ser Arg Ala Lys Ile Arg Arg Arg Lys Ala Ser Phe
 245 250 255
 Lys Arg Lys Glu Lys Asn Ser His Gln Lys Gly Tyr Gly Ile Thr Lys
 260 265 270
 Ser Glu Arg Thr Ser Arg Lys Arg Lys Arg Ala Arg Lys Lys Lys Ser
 275 280 285
 Phe Arg Asn Glu Glu
 290

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556

Gly Glu Thr Thr Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala
 1 5 10 15
 Ile Leu Cys Leu Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val
 20 25 30
 Val Lys Gln Lys Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile
 35 40 45
 Glu Lys Tyr Ser Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro
 50 55 60
 Phe Met Val Gln Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp
 65 70 75 80
 Asn Lys Gln Val Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys
 85 90 95
 Ile Thr Leu Ile Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr
 100 105 110
 Phe Gln Ala Asn Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro

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```

      115      120      125
Thr Leu Asn Gln Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp
      130      135      140
Asn Pro Asn Asn Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly
145      150      155      160
Ser Gln Pro Met Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp
      165      170      175
Val Ser Gly Ala Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu
      180      185      190
Lys Ala Gln Leu Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln
      195      200      205
Asp Lys Glu Gln Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile
210      215      220
Leu Glu Thr Leu Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val
225      230      235      240
Ile Ser Ser Glu Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys
      245      250      255
Glu Glu Glu Val Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr
      260      265      270
Leu Arg Asn Gln Ile Arg Ser Leu Leu Ser Gly Lys
      275      280

```

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557

```

Ser Tyr Cys Gln Met Lys Thr Leu Val Lys Asn Thr Ile Tyr Ser Phe
1      5      10
Leu Leu Leu Ser Val Leu Met Ala Glu Asp Ile Thr Ser Gly Leu Lys
      20      25      30
Gln Leu Asp Asn Thr Tyr Gln Glu Thr Asn Gln Gln Val Leu Lys Asn
      35      40      45
Leu Asp Glu Ile Phe Ser Thr Thr Ser Pro Ser Ala Asn Asn Lys Ile
      50      55      60
Gly Gln Glu Asp Ala Leu Asn Ile Lys Lys Ala Ala Ile Ala Leu Arg
      65      70      75      80
Gly Asp Leu Ala Leu Lys Ala Asn Phe Glu Ala Asn Glu Leu Phe
      85      90      95
Phe Ile Ser Glu Asp Val Ile Phe Lys Thr Tyr Met Ser Ser Pro Glu
      100      105      110
Leu Leu Leu Thr Tyr Met Lys Ile Asn Pro Leu Asp Gln Lys Thr Ala
      115      120      125
Glu Gln Gln Cys Gly Ile Ser Asp Lys Val Leu Val Leu Tyr Cys Glu
      130      135      140
Gly Lys Leu Lys Ile Glu Gln Glu Lys Gln Asn Ile Arg Glu Arg Leu
145      150      155      160
Glu Thr Ser Leu Lys Ala Tyr Gln Ser Asn Ile Gly Gly Thr Ala Ser
      165      170      175

```

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```

Leu Ile Thr Ala Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn
      180      185      190
Phe Ile Lys Gly Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe
      195      200      205
Leu Asn Tyr Leu Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln
      210      215      220
Ser Lys Arg Gln Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val
      225      230      235      240
Lys

```

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558

```

Ile Asn Lys Asn Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile
1      5      10      15
Ile Ser Phe Phe Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu
      20      25      30
Pro Ile Val Ser Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu
      35      40      45
Ile Pro Ser Tyr Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr
      50      55      60
Gly Tyr Thr Ser Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln
      65      70      75      80
Gly Val Ile Glu Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala
      85      90      95
Ser Asn Leu Val Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser
      100      105      110
Ala Trp Ala Ser Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro
      115      120      125
Ser Ser Gly Cys Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile
      130      135      140
Asp Val Ser Met Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln
      145      150      155      160
Asn Phe Thr Lys Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu
      165      170      175
Leu Gln Ile Ile Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr
      180      185      190
Ala Asp Gly Leu Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys
      195      200      205
Leu Gln Asn Asn Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser
      210      215      220
Val Val Lys Gly Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val
      225      230      235      240
Asn Leu Pro Asp Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val
      245      250      255
Ser Tyr Leu Ile Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe

```

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```

      260      265      270
Met Lys Leu Arg Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe
      275      280      285
Glu Tyr Met Arg Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val
      290      295      300
Ser Phe Ile Ala Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr
305      310      315      320
Ser Ile Tyr Phe Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu
      325      330      335
Phe Trp Ala Leu Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu
      340      345      350
Pro Ala Val Arg Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser
      355      360      365
Leu Leu Gln Gly Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe
      370      375      380
Met Gln Val Thr Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro
385      390      395      400
Leu Ile Ala Gly Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys
      405      410      415
Leu Ile Val Leu Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile
      420      425      430
Trp Phe Ile Asn Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu
      435      440      445
Leu Phe Gly Val Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro
      450      455      460
Ser Val Ala Ile Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser
465      470      475      480
Thr Ile Ala Ser Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu
      485      490      495
Thr Ile Ile Glu Ser Val Asn Ala Ile Val Asn Thr Ile Phe Ser Ser
      500      505      510
Val Ser Met Asp Gly Ser Arg Met Asp Arg Glu Arg Asp Ala Leu Met
      515      520      525
Val Gly Arg Val Gly Gly Ser Met Phe Lys Gly
530      535

```

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559

```

Leu His Arg Ile Ile Ser Cys Asp Ser Ala Trp Arg Thr Asn Leu Val
1      5      10      15
Val Arg Thr Asn Lys Ala Leu Tyr Gln Phe Ile Leu Arg Ile Ala Gln
      20      25      30
Lys Asp Asn Phe Ala Ser Ala Tyr Leu Thr Val Lys Leu Glu Tyr Pro
      35      40      45
Gln Arg His Glu Val Ser Ser Val Ile Glu Glu Glu Leu Lys Lys Arg
50      55      60

```

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```

Glu Glu Ala Lys Arg Gln Arg Glu Leu Ile Lys Gln Glu Asn Leu Asn
65      70      75      80
Thr Thr Ala Tyr Ile Asn Arg Val Met Met Ala Ser Asn Glu Gln Ile
      85      90      95
Ile Asn Lys Glu Lys Ile Arg Glu Glu Lys Gln Lys Ile Ile Leu Asp
      100      105      110
Gln Ala Lys Ala Leu Glu Thr Gln Tyr Val His Asn Ala Leu Lys Arg
      115      120      125
Asn Pro Val Pro Arg Asn Tyr Asn Tyr Tyr Gln Ala Pro Glu Lys Arg
      130      135      140
Ser Lys His Ile Met Pro Ser Glu Ile Phe Asp Asp Gly Thr Phe Thr
145      150      155      160
Tyr Phe Gly Phe Lys Asn Ile Thr Leu Gln Pro Ala Ile Phe Val Val
      165      170      175
Gln Pro Asp Gly Lys Leu Ser Met Thr Asp Ala Ala Ile Asp Pro Asn
      180      185      190
Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg Val Asn Glu Ile Ala Glu
      195      200      205
Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu Val Thr Val Ile Asn Lys
      210      215      220
Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn Tyr Asn Ile Lys Asn Tyr
225      230      235      240
Gly Glu Leu Glu Arg Val Ile Lys Lys Leu Pro Leu Val Arg Asp Lys
      245      250      255

```

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560

```

Thr Ser Ser Phe Lys Thr Lys Met Lys Arg Pro Ile Ser Lys Leu Lys
1      5      10      15
Gln Asn Phe Leu Gln Phe Lys His Ser Phe Asn Lys His Leu Asp Lys
      20      25      30
Tyr Ser Leu Tyr Tyr Arg Leu Phe Asn Ile Ser Ser Ile Val Ile Gly
      35      40      45
Phe Leu Ile Ala Leu Phe Ser Tyr Gly Ala Gly Val Ile Leu Val Tyr
      50      55      60
Pro Ile Leu Phe Leu Phe Ala Leu Ile Ile Lys Pro Ser Phe Phe Tyr
65      70      75      80
Tyr Thr Thr Tyr Leu Leu Leu Val Ser Leu Ser Ile Ile Ser Lys
      85      90      95
Tyr Tyr Leu Leu Ser His Ala Asn Phe Thr Met Lys Leu Ile Met Leu
      100      105      110
Met Thr Gln Trp Gln Asn Trp Phe Leu
      115      120

```

(2) INFORMATION FOR SEQ ID NO:1561:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561

```

Val Cys Tyr Cys Glu Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro
1          5          10          15
Asn Lys Gln Glu Leu Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly
20          25          30
Lys Ile Leu Ala Ser Leu Leu Gly Gly Thr Asn Leu Phe Thr Gly
35          40          45
Leu Ser Ser Asp Leu Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu
50          55          60
Met Leu Met Met Gly Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu
65          70          75          80
Pro Met Asp Asn Ile Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly
85          90          95
Phe Asp Ser Ile Lys Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe
100          105          110
Gly Ser Ser Lys Ser Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln
115          120          125
Val Arg Leu
130

```

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562

```

Glu Glu Leu Leu Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys
1          5          10          15
Phe Cys Leu Gly Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala
20          25          30
Leu Asp Ile Lys Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys
35          40          45

```

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```

Lys Ile Ala Tyr Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser
50      55      60
Leu Asp Asn Val Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser
65      70      75      80
Tyr Ile Thr Thr Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser
      85      90      95
Asn His Ile Phe Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe
      100      105      110
Glu Lys Glu Ala Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu
      115      120      125
Phe Leu Lys Thr Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu
130      135      140
Leu Glu Glu Gln Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu
145      150      155      160
Gln Ala Gln Lys Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu
      165      170      175
Arg Ala Lys Asn Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser
      180      185      190
Asn Pro Gln Asn Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys
      195      200      205
Gln Gln Arg Glu Asn Glu Leu Asp Gln Met Glu Arg Leu Glu Asp Met
210      215      220
Gln Glu Gln Ala Gln Ala Asn Ala Leu Lys Gln Ile Glu Glu Leu Asn
225      230      235      240
Lys Lys Gln Ala Glu Glu Ala Val Arg Gln Arg Ala Lys Asp Lys Ile
      245      250      255
Ser Ile Lys Thr Asp Lys Ser Gln Lys Ser Pro Glu Asp Asn Ser Ile
      260      265      270
Glu Leu Ser Pro Ala Ile Ala Leu Gly Gly Leu Ile Leu Leu Cys Gly
      275      280      285
Pro Ile Lys Pro Cys Ile Asn Ser Phe
290      295

```

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563

```

Ser Cys Arg Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu
1      5      10      15
Asn Leu Val Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn
      20      25      30
Lys Ala Asn Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu
      35      40      45
Asn Val Ala Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys
50      55      60
Thr Asp Ile Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys
65      70      75      80
Ile Val Lys Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val

```

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```

      85          90          95
Val Asp Ser Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser
      100          105          110
Lys Asn Ser Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp
      115          120          125
Val Ser Phe Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg
      130          135          140
Gln Phe Val Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile
      145          150          155          160
Gln Arg Glu Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe
      165          170          175
Ile Thr Ile Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile
      180          185          190
Thr Lys Lys Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser
      195          200          205
Ser Gln Glu Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp
      210          215          220
Ile Gln Ile Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu
      225          230          235          240
Arg Lys Ile Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
      245          250          255

```

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564

```

Lys Arg Leu Ile Gln Arg Asp Glu Thr Ile Ala Thr Gln Arg Glu Asn
1      5      10      15
Gly Ile Ile Ser Lys Gln Phe Leu Asn Leu Ile Leu Glu Arg Ser Phe
      20      25      30
Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro
      35      40      45
Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser
      50      55      60
Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu
      65      70      75      80
Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu
      85      90      95
Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys
      100     105     110
Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
      115     120     125
Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
      130     135     140
Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu
      145     150     155     160
Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala
      165     170     175

```

SUBSTITUTE SHEET (RULE 26)

1119

```

Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser
      180      185      190
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
      195      200      205
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
      210      215      220
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
      225      230      235      240
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565

```

Gly Tyr Lys Asn Tyr Lys Met Leu Ala Lys Ile Val Phe Ser Ser Leu
1      5      10      15
Val Ala Phe Gly Val Leu Ser Ala Asn Val Glu Gln Phe Gly Ser Phe
      20      25      30
Phe Asn Glu Ile Lys Lys Glu Gln Glu Val Ala Ala Lys Glu Asp
      35      40      45
Ala Leu Lys Ala Arg Lys Lys Leu Leu Asn Asn Thr His Asp Phe Leu
      50      55      60
Glu Asp Leu Val Phe Arg Lys Lys Ile Lys Glu Leu Val Asp Tyr
      65      70      75      80
Arg Ala Lys Val Leu Leu Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys
      85      90      95
Glu Ala Leu Glu Lys Glu Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser
      100      105      110
Lys Ala Tyr Gly Asp Leu Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr
      115      120      125
Lys Lys Leu Leu Pro Asn Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr
      130      135      140
Phe Thr Gln Glu Asp Lys Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val
      145      150      155      160
Lys Thr Ser Ser Ile Phe Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys
      165      170      175
Ala Gln Ala Leu Leu Gln Met Gly Val Phe Ser Leu Asp Glu Glu Gln
      180      185      190
Asn Lys Lys Ala Ser Arg Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu
      195      200      205
Glu Tyr Ser Asn Asn Ile Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp
      210      215      220
Asn Ile Asp Tyr Tyr Leu Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys
      225      230      235      240
Ala Lys Asp Ile Ala Gln Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser
      245      250      255
Glu Arg Leu Ala Phe Ser Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr

```

SUBSTITUTE SHEET (RULE 26)

1120

```

      260      265      270
Leu Arg Gly Tyr Glu Ala Phe Ser Asn Leu Leu Lys Asn Val Lys Asp
      275      280      285
Asp Val Glu Leu Asn Thr Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu
      290      295      300
Ser Phe Ala Gln Lys Gln Lys Leu Cys Leu Leu Val Leu Asp Ser Phe
      305      310      315      320
Asn Phe Asp Thr Gln Ser Lys Lys Ser Ile Leu Lys Lys Thr Asn Glu
      325      330      335
Tyr Asn Ile Phe Val Asp Ser Asp Pro Met Met Ser Asp Lys Thr Thr
      340      345      350
Met Gln Lys Glu His Tyr Lys Ile Phe Asn Phe Phe Lys Thr Val Val
      355      360      365
Ser Ala Tyr Arg Asn Asn Val Ala Lys Asn Asn Pro Phe Glu
      370      375      380

```

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566

```

Lys Phe Ser Glu Val Tyr Phe Ile Met Lys Thr Lys Ala Gly Phe Val
1      5      10      15
Ala Leu Ile Gly Lys Pro Asn Ala Gly Lys Ser Thr Leu Leu Asn Thr
      20      25      30
Leu Leu Asn Ala His Leu Ala Leu Val Ser His Lys Ala Asn Ala Thr
      35      40      45
Arg Lys Leu Met Lys Cys Ile Val Pro Phe Lys Asp Lys Glu Gly Tyr
      50      55      60
Glu Ser Gln Ile Ile Phe Leu Asp Thr Pro Gly Leu His His Gln Glu
      65      70      75      80
Lys Leu Leu Asn Gln Cys Met Leu Ser Gln Ala Leu Lys Ala Met Gly
      85      90      95
Asp Ala Glu Leu Arg Val Phe Leu Ala Ser Val His Asp Asp Leu Lys
      100      105      110
Gly Tyr Glu Glu Phe Leu Ser Leu Cys Gln Lys Pro His Ile Leu Ala
      115      120      125
Leu Ser Lys Ile Asp Thr Ala Thr His Lys Gln Val Leu Gln Lys Leu
      130      135      140
Gln Glu Tyr Gln Lys Tyr Ser Ser Gln Phe Leu Ala Leu Val Pro Leu
      145      150      155      160
Ser Ala Lys Lys Ser Gln Asn Leu Asn Ala Leu Leu Glu Cys Ile Ser
      165      170      175
Lys His Leu Ser Pro Ser Ala Trp Leu Phe Glu Lys Asp Leu Met Ser
      180      185      190
Asp Glu Lys Met Arg Asp Ile Tyr Lys Glu Ile Ile Arg Glu Ser Leu
      195      200      205
Phe Asp Phe Leu Ser Asp Glu Ile Pro Tyr Glu Ser Asp Val Met Ile
      210      215      220

```

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1121

Asp Lys Phe Ile Glu Glu Glu Arg Ile Asp Lys Val Tyr Ala Arg Ile
 225 230 235 240
 Ile Val Glu Lys Glu Ser Gln Lys Lys Ile Val Ile Gly Lys Asn Gly
 245 250 255
 Val Asn Ile Lys Arg Ile Gly Thr Asn Ala Arg Leu Lys Met Gln Glu
 260 265 270
 Val Gly Glu Lys Lys Val Phe Leu Asn Leu Gln Val Ile Ala Gln Lys
 275 280 285
 Ser Trp Ser Lys Glu Glu Lys Ser Leu Gln Lys Leu Gly Tyr Ile Tyr
 290 295 300
 Gln Arg Asn Arg Asp
 305

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567

Phe Leu Ser Leu Ser Leu Ile Glu Arg Asp Leu Lys Thr Met Ala Lys
 1 5 10 15
 Ile Leu Lys Pro Asn Leu Asp Arg Asp Glu Leu Asn Thr Leu Tyr Lys
 20 25 30
 Ala Asn Leu Ala Tyr Ala Lys Asn Thr His Glu His Tyr Phe Lys Phe
 35 40 45
 Lys Lys Asp Val Asp Tyr Lys Leu Phe Asn Pro Ser Ile Met His Glu
 50 55 60
 Gln Cys Ser Ile Ser Phe Val Gly Gly Gln Gly Ala Lys Arg Leu Leu
 65 70 75 80
 Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn Lys Ile Ala
 85 90 95
 Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val Ala Arg Thr
 100 105 110
 Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe Ile Glu Val
 115 120 125
 Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys Asp Tyr Arg
 130 135 140
 Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr Val Met Tyr
 145 150 155 160
 Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg Tyr Gly Phe
 165 170 175
 Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys Glu Ser Leu
 180 185 190
 Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu Lys Thr Leu
 195 200 205
 Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn Lys Cys Ile
 210 215 220
 Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu Val Leu Asn
 225 230 235 240
 Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr Ser Ile Leu

SUBSTITUTE SHEET (RULE 26)

1122

245 250 255
 Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile Lys Lys Ser
 260 265 270
 Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp Tyr Arg Leu
 275 280 285
 Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys Gln Lys Ser
 290 295 300
 Gln Asn Ser Leu Thr Leu Tyr Asn Phe Ile Pro Leu Ile Phe Lys Leu
 305 310 315 320
 Ala Gln Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe
 325 330 335
 Arg His Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val
 340 345 350
 Leu Thr Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile
 355 360 365
 Tyr Ile His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe
 370 375 380
 Asp Ser Leu Ile Glu Asn Lys Lys
 385 390

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568

Lys Arg Lys Glu His Cys Met Lys Asn Leu Arg His Phe Arg Lys Leu
 1 5 10 15
 Ile Ala Phe Leu Gly Phe Ser Pro Leu Leu Leu Gln Ala Asp Met Thr
 20 25 30
 Thr Phe Phe Asn Ser Ile Glu Gln Leu Thr Ser Pro Thr Ala Lys
 35 40 45
 Gly Ile Leu Met Val Ile Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys
 50 55 60
 Asn Leu Asp Arg Trp Lys Glu Ile Leu Met Thr Val Leu Ala Leu Lys
 65 70 75 80
 Glu Val Pro Met Gln Leu Val Ala Ile Ser Val Ser Asn Leu Lys Glu
 85 90 95
 Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu
 100 105 110
 Leu Ser Gly Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu
 115 120 125
 Asn Ser Phe Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala
 130 135 140
 Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys
 145 150 155 160
 Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala
 165 170

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1123

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569

```

Lys Ser Arg Asn Phe Ser Tyr Asn Gln Thr Glu Lys Ile Trp Glu Asn
1      5      10      15
His Phe Asn Leu Phe Ser Val Gly Ile Gly Met Ala Glu Glu Gln Glu
20      25      30
Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser Lys Ala Leu Leu Phe Val
35      40      45
Ile Ile Gly Ser Val Leu Val Met Leu Leu Leu Val Gly Val Ile Ile
50      55      60
Met Leu Leu Met Gly Asn Lys Glu Glu Ser Lys Glu Asn Ala Ser Lys
65      70      75      80
Asn Thr Gln Glu Val Gln Ala Asn Pro Met Ala Asn Lys Asn Gln Glu
85      90      95
Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr Leu Val Leu Gly Pro Leu
100      105      110
Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn Leu Val Ser Gln Asn Gly
115      120      125
Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu Glu Leu Ser Asn Glu Lys
130      135      140
Leu Leu Asn Glu Val Lys Val Lys Asp Thr Ala Ile Lys Asp Thr Ile
145      150      155      160
Ile Glu Ile Leu Ser Ser Lys Ser Val Glu Glu Val Val Thr Asn Lys
165      170      175
Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys Ser His Leu Asn Ser Phe
180      185      190
Leu Ile Asp Gly Phe Ile Lys Asn Val Phe Phe Thr Asp Phe Ile Ile
195      200      205
Gln

```

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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1124

(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570

```

Gly Ser Met Met Thr Glu Met Glu Leu Lys Leu Ile Lys Ile Asp Thr
1          5          10          15
Ser His Tyr Phe Glu Lys Lys Pro Gly Leu Gly Glu Arg Met Asp Tyr
20          25          30
Ala Gly Arg Cys Tyr Tyr Asn Lys Phe Gln Arg Val Asn Ala Met Leu
35          40          45
Thr Ser Ser Leu Ile Gln Lys His Leu Lys Arg Glu Ile Glu Ile Ala
50          55          60
His Asn Leu Ile Leu Arg Asn Asp Lys Val Glu Asn Ile Val Phe Asp
65          70          75          80
Tyr Asn Gly Arg Asn Pro Glu Arg Phe Tyr His Lys Ala Gln Leu Leu
85          90          95
Leu Arg Glu Glu Gly Phe Met Asn Phe Thr Ala Tyr Asn Thr Lys Thr
100          105          110
Pro Gly His Leu His Leu Tyr Val His Lys Gly His Thr Glu Leu Gly
115          120          125
Glu Gly Glu Arg Leu Ile Lys Thr Leu Ser Met Lys Leu Ala Gln Gly
130          135          140
Leu Pro Lys Glu Trp Arg Val Phe Pro Ser Asn Glu Trp Pro Lys Glu
145          150          155          160
Phe Asn Ile Leu Ala Leu Pro Tyr Glu Val Phe Ala Lys Glu Arg Gly
165          170          175
Ser Ser Trp Ala Lys His Leu
180

```

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571

```

Pro Phe Leu Lys Gly Phe Leu Met Ser Glu Lys Glu Arg Leu Asn Glu
1          5          10          15
Val Ile Leu Glu Glu Glu Asn Asn Gly Ser Gly Thr Lys Lys Val Phe
20          25          30
Leu Ile Val Ala Ile Ala Ile Ile Ile Leu Ala Val Leu Leu Met Val
35          40          45
Phe Trp Lys Ser Thr Arg Val Ala Pro Lys Glu Thr Phe Leu Gln Thr
50          55          60
Asp Ser Gly Met Gln Lys Ile Gly Asn Thr Lys Asp Glu Lys Lys Asp
65          70          75          80
Asp Glu Phe Glu Ser Leu Asn Met Asp Ser Pro Lys Gln Glu Asp Lys
85          90          95
Leu Asp Lys Val Val Asp Asn Ile Lys Lys Gln Glu Ser Glu Asn Ser
100          105          110

```

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1125

Met Pro Ile Gln Thr Asp Gln Ala Gln Met Glu Met Lys Thr Thr Glu
 115 120 125
 Glu Lys Gln Glu Ser Gln Lys Glu Leu Lys Ala Val Glu Pro Ile Pro
 130 135 140
 Met Ser Thr Gln Lys Glu Ser Gln Ala Val Ala Lys Lys Glu Thr Pro
 145 150 155 160
 His Lys Lys Pro Lys Val Ala Pro Lys Asp Lys Glu Ala His Lys Asp
 165 170 175
 Lys Ala Lys His Ala Ala Lys Glu Pro Lys Val Lys Lys Glu Ala Arg
 180 185 190
 Lys Glu Val Ser Lys Lys Ala Asn Ser Lys Thr Asn Leu Thr Lys Gly
 195 200 205
 His Tyr Leu Gln Val Gly Val Phe Ala His Thr Pro Asn Lys Ala Phe
 210 215 220
 Leu Gln Glu Phe Asn Gln Phe Pro His Lys Ile Glu Asp Arg Gly Ala
 225 230 235 240
 Thr Lys Arg Tyr Leu Ile Gly Pro Tyr Lys Ser Lys Gln Glu Ala Leu
 245 250 255
 Met His Ala Asp Glu Val Ser Lys Lys Met Thr Lys Pro Val Val Ile
 260 265 270
 Glu Val Arg
 275

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572

Ser Arg Leu Gln Lys Ala Ile Ile Lys Arg Val Glu Met Leu Glu Lys
 1 5 10 15
 Leu Ile Glu Arg Val Leu Phe Ala Thr Arg Trp Leu Leu Ala Pro Leu
 20 25 30
 Cys Ile Ala Met Ser Leu Val Leu Val Val Leu Gly Tyr Val Phe Met
 35 40 45
 Lys Glu Leu Trp His Met Leu Ser His Leu Asp Thr Ile Ser Glu Thr
 50 55 60
 Asp Leu Val Leu Ser Ala Leu Gly Leu Val Asp Leu Leu Phe Met Ala
 65 70 75 80
 Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe Val Ser
 85 90 95
 Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys His Thr
 100 105 110
 Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val Ala Ile
 115 120 125
 Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp Val Leu
 130 135 140
 Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile Phe Trp
 145 150 155 160
 Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu Thr Ala

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1126

Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
 165 170 175
 180 185

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573

Gly Leu Asn Tyr Ile Asp Leu Ala Leu Leu Val Val Val Val Ala Phe
 1 5 10 15
 Gly Ile Arg Gly Phe Tyr His Gly Phe Val Ser Glu Ile Ala Ala Thr
 20 25 30
 Leu Gly Ile Val Leu Gly Val Tyr Leu Ala Ser Arg Tyr Ser Val Ala
 35 40 45
 Val Gly Asn Leu Phe Ser Glu His Leu Tyr Asp Leu Arg Asn Glu Thr
 50 55 60
 Met Thr Asn Leu Ile Gly Phe Leu Leu Val Leu Ala Ser Ile Trp Val
 65 70 75 80
 Phe Phe Leu Ala Leu Gly Val Leu Leu Gly Lys Met Leu Val Phe Ser
 85 90 95
 Gly Leu Gly Ile Ile Asp Lys Ala Leu Gly Phe Ile Phe Ser Cys Leu
 100 105 110
 Lys Thr Phe Leu Val Leu Ser Phe Ile Leu Tyr Ala Leu Ser Lys Met
 115 120 125
 Asp Leu Met Lys Asp Ala Asn Ala Tyr Leu Gln Glu Lys Ser Ala Ile
 130 135 140
 Phe Pro Thr Met Lys Ser Val Ala Ser Lys Ile Met Arg Leu Asp Gly
 145 150 155 160
 Val Lys His Val Glu Lys Asn Leu Lys Asp Asn Leu Glu Glu Met Ser
 165 170 175
 Asp Glu Val Lys Asn Lys Gly Ser Ile Asp Asn Ala Lys Glu Ser Phe
 180 185 190
 Asn Lys Ala Thr Asp Lys Gly Val Glu Ala Leu Lys Glu Lys Ala Lys
 195 200 205
 Asp Leu Pro Lys Asn Met Leu Glu Pro Lys His Asn Lys Pro Asn Gln
 210 215 220
 Thr Pro Pro Ile Pro Thr Pro Ser Asn Lys Glu Pro Leu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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1127

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574

```

Ser Leu Trp Val Glu Asn Pro Ile Leu Leu Ser His Ser Gln Val Tyr
1      5      10      15
Ser Pro Pro Arg Cys Trp Val Phe Lys Thr Pro Arg Asn Ser Ala Phe
20      25      30
Ala Leu Gly Phe Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu
35      40      45
Arg Leu Ser His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val
50      55      60
Leu Val Ala Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Tyr Phe
65      70      75      80
Glu Asn Pro Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile
85      90      95
His Pro Phe Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr
100     105     110
Ser Val Phe Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala
115     120     125
Cys Ile Phe Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly
130     135     140
Val Leu Leu Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser
145     150     155     160
Asp Leu Lys Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro
165     170     175
Gln Asp Leu Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn
180     185     190
Ile Leu Lys Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile
195     200     205
Val Phe Pro Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe
210     215     220
Lys Thr Gln Leu Glu Asp Leu Ser Ala Lys Ile Ala Ile Leu Ile Gly
225     230     235     240
Thr Leu Arg Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe
245     250     255
Ser Lys Lys Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe
260     265     270
Gly Glu Ile Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys
275     280     285
Leu Phe Phe Gly Glu Ser Ala Tyr Leu Tyr Arg Asn Ala Pro His Phe
290     295     300
Ser Asp Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr
305     310     315     320
Glu Gly Thr Ser Lys Pro Ala Tyr Ser Ser Ser Pro Ser Lys Val Phe
325     330     335
Ile Leu Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr
340     345     350
Leu Gln Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile
355     360     365
Ile Leu His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser
370     375     380
Leu Leu Gly Asp Ile Leu Phe Arg Lys Arg Ser
385     390     395

```

(2) INFORMATION FOR SEQ ID NO:1575:

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1128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575

```

Glu Thr Ile Met Ile Lys Ala Ile Asp Ile Ser His Ala Phe Glu Lys
1           5           10           15
Pro Leu Tyr Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Leu
          20           25           30
Ala Ile Leu Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ser His
          35           40           45
Leu Ala Thr Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu
          50           55           60
His Gln Asp Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg
65           70           75           80
Arg Leu Lys Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly
          85           90           95
Phe Ser Ala Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln
          100          105          110
Glu Ile Asn His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu
          115          120          125
Lys Gln Gly Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Leu Ser
          130          135          140
Ile Ala Arg Val Leu Ser Lys Lys Pro Gln Ile Ile Ile Ala Asp Glu
145          150          155          160
Pro Thr Gly Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met
          165          170          175
Leu Gln Asn Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr
          180          185          190
His Asp Glu His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu
          195          200          205
Lys Glu Ser Leu Ile Lys Glu Lys
210          215

```

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576

```

Ser Leu Ala Pro Lys Leu Lys Ala Phe Phe Lys Val Ala Leu Ser Cys
1           5           10           15
Lys Ala Val Ile Lys Ile Thr Gly Val Glu Ile Lys Lys Ser Phe Leu
20           25           30
Met Arg Leu Asn Asn Ser Lys Leu Phe Ile Ser Gly Thr Cys Thr Ser
35           40           45
Lys Ser Lys Arg Leu Lys Arg Ser Thr Glu Ser Leu Ser
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577

```

Phe Ala Leu His Lys Lys Val Leu Leu Ala Leu Thr Ala Ser Leu Ile
1           5           10           15
Cys Gln Glu Ser Leu Phe Ala Lys Asp Lys Asp Tyr Thr Leu Gly Lys
20           25           30
Val Ser Thr Ala Gly Lys Lys Asp Arg Ser Asp Tyr Ser Gly Gln Val
35           40           45
Asn Leu Gly Tyr Ser Gly Ile Thr Ala Pro Lys Ser Trp Gln Asp Glu
50           55           60
Glu Val Lys Lys Tyr Thr Gly Ser Arg Thr Val Ile Ser Asn Lys Ala
65           70           75           80
Leu Thr Gln Gln Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val
85           90           95
Pro Gly Leu Gln Ile Arg Asn Ala Thr Gly Val Gly Ala Met Pro Thr
100          105          110
Ile Gln Ile Arg Gly Phe Gly Ala Gly Ser Gly His Ser Asp Ala
115          120          125
Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala Pro Tyr Ala
130          135          140
His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala Ile Asp Arg
145          150          155          160
Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly Pro Asn Thr
165          170          175
Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro Asn Gln Trp
180          185          190
Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys Ala Arg Asn
195          200          205
Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro Ser Phe Ile
210          215          220
Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val Arg Ser Gly
225          230          235          240
Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala Asn Trp Val

```

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```

                245                250                255
Arg Gly Gln Gly Phe Arg Asp Asn Ser Ser Ser Ile Ser Asn Tyr
                260                265                270
Trp Leu Asp Gly Val Tyr Asp Ile Asn Glu Ser Asn Gly Ile Lys Ala
                275                280                285
Tyr Tyr Gln Tyr Tyr Asp Phe Ala Ile Ala Gln Pro
                290                295                300

```

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578

```

Val Ser Ile Leu Val Ile Ile Glu Pro Tyr Thr Phe Tyr Lys Arg Glu
1          5          10          15
Glu Ser Val Met Leu Gly Ser Val Lys Lys Ala Val Phe Arg Val Leu
          20          25          30
Cys Leu Gly Ala Leu Cys Leu Cys Gly Gly Leu Met Ala Glu Gln Asp
          35          40          45
Pro Lys Glu Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn
          50          55          60
Phe Thr Arg Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp
          65          70          75          80
Ala Asp Gly Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala
          85          90          95
Ile Ala Arg Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His
          100         105         110
Thr Ala Thr Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys
          115         120         125
Asp Leu Ala Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu
          130         135         140
Glu Tyr Tyr Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met
          145         150         155         160
Leu Ser Ala Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp
          165         170         175
Lys Lys Asp Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly
          180         185         190
Gly Gly Cys Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val
          195         200         205
Thr Lys Asp Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu
          210         215         220
Leu Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu
          225         230         235         240
Gly Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu
          245         250         255
Lys Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu
          260         265         270
Gln Lys Gln
          275

```

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(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579

```

Thr Arg Lys Ser Ser Ala Ser Met Ser Glu Asn Glu Lys His Pro His
1          5          10          15
Arg Val Leu Gln Leu Ile Lys Ser Ser Gly Ile Thr Pro Gly Ile Val
          20          25          30
Leu Asn Pro His Thr His Glu Glu Ser Ile Lys Tyr Leu Leu Glu Ser
          35          40          45
Val Gly Leu Val Leu Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln
          50          55          60
Lys Phe Leu Asp Leu Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu
          65          70          75          80
Ile Lys Arg Tyr Asn Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val
          85          90          95
Asn Asp Lys Asn Ile Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val
          100          105          110
Val Ser Gly Ser Tyr Ile Phe Glu Ser Lys Asp Arg Lys Leu Ala Ile
          115          120          125
Glu Gly Leu Gln Asn Val Arg Gln Pro Leu Ala
          130          135

```

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580

```

Lys Leu Leu Arg Val Leu His Lys Met Ile Lys Lys Ala Ala Lys Thr
1          5          10          15
Pro Phe Phe Lys Ile Leu Phe Gln Ala Leu Ser Tyr Asn Ile Arg Met

```

SUBSTITUTE SHEET (RULE 26)

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Lys | Asp | Leu | Asn | Lys | Thr | Ile | Gly | Val | Phe | Val | Arg | Pro | Thr | His | His | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Gln | Asn | Ala | Leu | Phe | Lys | Glu | Leu | Glu | Gln | Ala | Lys | Glu | Trp | Val | Leu | |
| | | 50 | | | | 55 | | | | | 60 | | | | | |
| Thr | Leu | Leu | Glu | Asp | Glu | Gly | Phe | Glu | Ser | Phe | Met | Ile | Asp | Ser | Leu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Gly | Ala | Lys | Asp | Ala | Gln | Leu | Ile | Lys | Lys | Ala | Tyr | Ala | Phe | Leu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Cys | Leu | Gly | Gly | Asp | Gly | Thr | Ile | Leu | Gly | Ala | Leu | Arg | Met | Thr | His | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ala | His | Asn | Lys | Pro | Cys | Phe | Gly | Val | Arg | Ile | Gly | Asn | Leu | Gly | Phe | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Leu | Ser | Ala | Val | Glu | Leu | Asn | Gly | Leu | Lys | Asp | Phe | Leu | Gln | Asp | Leu | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Lys | Gln | Asn | Arg | Ile | Lys | Leu | Glu | Glu | His | Leu | Ala | Leu | Glu | Gly | Arg | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ile | Gly | Asn | Thr | Ser | Phe | Tyr | Ala | Ile | Asn | Glu | Ile | Val | Ile | Ala | Lys | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Lys | Lys | Ala | Leu | Gly | Val | Leu | Asp | Ile | Lys | Ala | Cys | Ala | Gly | His | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Pro | Phe | Asn | Thr | Tyr | Lys | Gly | Asp | Gly | Leu | Ile | Ile | Ala | Thr | Pro | Leu | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| Gly | Ser | Thr | Ala | Tyr | Asn | Leu | Ser | Ala | His | Gly | Pro | Ile | Val | His | Ala | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Leu | Ser | Gln | Ser | Tyr | Ile | Leu | Thr | Pro | Leu | Cys | Asp | Phe | Ser | Leu | Thr | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Gln | Arg | Pro | Leu | Val | Leu | Gly | Ala | Glu | Phe | Cys | Leu | Ser | Phe | Cys | Ala | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| His | Glu | Asp | Ala | Leu | Val | Val | Ile | Asp | Gly | Gln | Ala | Thr | Tyr | Asp | Leu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Lys | Ala | Asn | Gln | Pro | Leu | Tyr | Ile | Gln | Lys | Ser | Pro | Thr | Thr | Thr | Lys | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Leu | Leu | Gln | Lys | Asn | Ser | Arg | Asp | Tyr | Phe | Lys | Val | Leu | Lys | Glu | Lys | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| Leu | Leu | Trp | Gly | Glu | Ser | Pro | Asn | Lys | Lys | Arg | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | |

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...218
```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Asn | Thr | Pro | Met | Gln | Lys | Lys | Ile | Phe | Leu | Leu | Glu | Asp | Asp |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Tyr | Leu | Leu | Ser | Glu | Ser | Ile | Lys | Glu | Phe | Leu | Glu | His | Leu | Gly | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Val | Phe | Cys | Ala | Phe | Asn | Gly | Lys | Glu | Ala | His | Glu | Arg | Leu | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |

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Val Glu Arg Phe Asn Leu Leu Leu Asp Val Gln Val Pro Glu Met
 50 55 60
 Asn Ser Leu Glu Leu Phe Lys Arg Ile Lys Asn Asp Phe Leu Ile Ser
 65 70 75 80
 Thr Pro Val Ile Phe Ile Thr Ala Leu Gln Asp Asn Ala Thr Leu Lys
 85 90 95
 Asn Ala Phe Asn Leu Gly Ala Ser Asp Tyr Leu Lys Lys Pro Phe Asp
 100 105 110
 Leu Asp Glu Leu Glu Ala Arg Ile Lys Arg Phe Phe Asn Asp Asp Pro
 115 120 125
 Ile Glu Ile Met Pro Asn Ile Phe Tyr His Gln His Ala Leu Asn Val
 130 135 140
 Lys Gly Lys Lys Glu Ile Leu Ala Pro Lys Thr Ala Gln Leu Leu Glu
 145 150 155 160
 Tyr Phe Leu Glu His Lys Gly Gln Ile Ile Ser Ser Gln Ala Leu Glu
 165 170 175
 Asn Asn Leu Trp Glu Gln Ala Ile Asp Asp Ser Thr Leu Arg Thr Tyr
 180 185 190
 Ile Lys Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His
 195 200 205
 Lys Gly Val Gly Tyr Arg Phe Asn Pro Leu
 210 215

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582

Cys Gly Ala Asn Arg Ser Lys Gly Arg Gly Gly Phe Ser Ser Lys Cys
 1 5 10 15
 Ala Gly Ala Asn Ser Gly Tyr Ser Asn Glu Ala Tyr Glu Ser Val Gly
 20 25 30
 Ala Lys Ile Val Asp Ser Lys Thr Ala Trp Gly Gln Asp Leu Val Val
 35 40 45
 Lys Cys Lys Glu Pro Leu Glu His Glu Tyr Pro Leu Leu Lys Glu Lys
 50 55 60
 Ala Thr Leu Phe Ser Tyr Leu Asp Leu Ala Tyr Gln Lys Ser Leu Cys
 65 70 75 80
 Glu Met Phe Ile Asn Lys Lys Ile Thr Ser Ile Cys Thr Glu Thr Ile
 85 90 95
 Ala Gly Pro Lys Asn Asp Tyr Pro Ile Leu Ala Pro Met Ser Val Val
 100 105 110
 Ala Gly Arg Leu Ala Ala His Leu Val Gln His Tyr Leu Leu Ala Leu
 115 120 125
 Glu His Val Lys Gly Phe Met Gly Lys Gly Val Met Leu Gly Gly Leu
 130 135 140
 Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val Val
 145 150 155 160
 Gly Met Glu Ser Ala Lys Val Leu Ser Gln Met Gly Ala Lys Val Thr

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```

      165      170      175
Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr His
      180      185      190
Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile Gln
      195      200      205
Ala Leu Asn Gly Ala Val Gly Leu Val Gly Ala Val Leu Val Thr Ala
      210      215      220
Ser Gln Thr Pro Lys Val Ile Leu Arg Arg His Leu Lys Tyr Met Gln
      225      230      235
Thr Gln Gly Val Val Ile Asp Val Ala Cys Ser Leu Gly Gly Cys Ile
      245      250      255
Arg Ala Ile Arg Gln Ala Ser His Ser Asn Pro Val Tyr Val Glu Glu
      260      265      270
Ser Leu Leu His Tyr Gly Val Pro Asn Met Pro Gly Ile Val Ala Lys
      275      280      285
Thr Ser Ser Thr Ala Tyr Ser His Ala Ser Val Pro Tyr Leu Leu Tyr
      290      295      300
Tyr Leu Glu His Gly Leu Lys Gly Phe Leu Thr Ala Asn Thr Lys Ile
      305      310      315
Val Ala Asn Thr Leu Gly Gly Leu Ser Ala Tyr Asn Gly Tyr Ile Thr
      325      330      335
Gln Glu Gly Ile Ala Lys Ala Phe Asn Leu Ala Phe Lys Ser Pro Leu
      340      345      350
Glu Ile Leu Lys Glu Leu
      355

```

(2) INFORMATION FOR SEQ ID NO:1583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583

```

Lys Gly Lys Arg Val Lys Asn Met Arg Asp Phe Asn Asn Ile Gln Ile
1      5      10      15
Thr Arg Leu Lys Val Arg Gln Asn Ala Val Phe Glu Lys Leu Asp Leu
      20      25      30
Glu Phe Lys Asp Gly Leu Ser Ala Ile Ser Gly Ala Ser Gly Val Gly
      35      40      45
Lys Ser Val Leu Ile Ala Ser Leu Leu Gly Ala Phe Gly Leu Lys Glu
      50      55      60
Ser Asn Ala Ser Asn Ile Glu Val Glu Leu Ile Ala Pro Phe Leu Asp
      65      70      75      80
Thr Glu Glu Tyr Gly Ile Phe Arg Glu Asp Glu His Glu Pro Leu Val
      85      90      95
Ile Ser Val Ile Lys Lys Glu Lys Thr Arg Tyr Phe Leu Asn Gln Thr
      100      105      110
Ser Leu Ser Lys Asn Thr Leu Lys Ala Leu Leu Lys Gly Leu Ile Lys
      115      120      125
Arg Leu Ser Asn Asp Arg Phe Ser Gln Asn Glu Leu Asn Asp Ile Leu
      130      135      140

```

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Met Leu Ser Leu Leu Asp Gly Tyr Ile Gln Asn Lys Asn Arg Arg Leu
 145 150 155 160
 Ala Pro Phe

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584

Ser Asn His Lys Arg Val Phe Met Asp Tyr Lys Arg Phe Lys Gly Lys
 1 5 10 15
 His Ala Asn Ile Val Ile Glu Ile Ile Ser Leu Leu Glu Lys Gly Val
 20 25 30
 Lys Lys Ala Gln Glu Ile Leu Glu Lys Pro Asp Ala Gly Ser Tyr Thr
 35 40 45
 Gln Leu Glu Asn Ser Ser Gly Asp Thr Pro Ile Lys Ala Asp Leu Ala
 50 55 60
 Leu Asp Lys Phe Leu Glu Thr Phe Leu Ser Leu Glu Asn Val Lys
 65 70 75 80
 Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu Asn Gly
 85 90 95
 Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val Met Glu
 100 105 110
 Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys Asp Tyr
 115 120 125
 Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly His Lys
 130 135 140
 Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala Phe Tyr
 145 150 155 160
 Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn Lys Gly
 165 170 175
 Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu Gly Leu
 180 185 190
 Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu Arg Tyr
 195 200 205
 Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys Lys Gly
 210 215 220
 Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe Glu Val
 225 230 235 240
 Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala Phe Tyr
 245 250 255
 Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val Glu Ser
 260 265 270
 Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu Ala Gln
 275 280 285
 Ile Leu Glu Lys His Leu Lys Gly Glu
 290 295

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(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585

```

Thr Phe Leu Ile Ile Phe Trp Val Phe Phe Leu Arg Ile Lys His Tyr
1      5      10      15
Val Lys Glu Leu Ser Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala
20      25      30
Leu Ile Ile Ser Met Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val
35      40      45
Phe Leu Gly Ala Gly Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp
50      55      60
Ile Asn Ser Gln Lys Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp
65      70      75      80
Ala Leu Leu Gly Tyr Gln Phe Phe Phe Glu Lys His Phe Gly Leu Arg
85      90      95
Leu Tyr Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile Lys Leu Lys
100     105     110
Asn Pro Asn Tyr Asn Ser Glu Ala Ala Gln Val Ala Ser Gln Ile Leu
115     120     125
Gly Lys Gln Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp Pro Arg Thr
130     135     140
Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val
145     150     155     160
Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Ile
165     170     175
Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly
180     185     190
Ile Leu Val Glu Gln Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln
195     200     205
Phe Leu Phe Asn Val Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser
210     215     220
Ile Glu Ala Gly Val Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile
225     230     235     240
Thr Ala Lys Asn Leu Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr
245     250     255
Val Asn Tyr Val Phe Thr Phe
260

```

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586

```

Trp Ile Asp Ala Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly Tyr Thr
1      5      10
Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu Leu Val
20     25     30
Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser Leu
35     40     45
Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser Lys
50     55     60
Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu His
65     70     75     80
Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile Thr
85     90     95
Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu Gln
100    105    110
Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser Glu
115    120    125
Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu Gln Phe
130    135    140
Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu Leu Leu
145    150    155    160
Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Gly Val Ser Glu Glu Ala
165    170    175
Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile Val Glu
180    185    190
Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala Arg Ile
195    200    205
Asp Val Val Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser Asn Phe
210    215    220
Glu Ala Leu Gly Thr Ile His Ile Asn Phe
225    230

```

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587

Lys Lys Lys Thr Leu Asn Ile Ser Gln Leu Gly Lys Thr Met His Val

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```

1           5           10           15
Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu Ser Leu Leu
20           25           30
Lys Glu Ile Ala Ser Lys Gln Gln Ser Leu Lys Ile Leu Gly Thr
35           40           45
His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu Lys His Phe
50           55           60
Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr Asp Leu Lys
65           70           75           80
Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp Leu Leu Lys
85           90           95
Ala Ile Lys Lys His Gln Ile Lys Arg Leu Ile Leu Glu Lys Gln Asp
100          105          110
Phe Arg Ser Phe Leu Leu Ser Gln Phe Val Ser Ile Thr Thr Pro Asn
115          120          125
Lys Glu Ile Lys Asn Val Tyr Gln Asn Arg Gln Glu Leu Phe Ser Gln
130          135          140
Ile Tyr Gly His Val Phe Asp Asn Pro Pro Tyr Pro Met Ser Leu Lys
145          150          155          160
Asn Pro Lys Lys Ile Leu Ile Asn Pro Phe Thr Arg Glu Asn Asp Arg
165          170          175
Asn Ile Ser Leu Glu His Leu Lys Ile Val Leu Lys Leu Leu Lys Pro
180          185          190
Phe Cys Val Thr Leu Leu Asp Phe Glu Glu Arg Tyr Ala Phe Leu Lys
195          200          205
Asp Arg Val Ala His Tyr Arg Ala Lys Thr Ser Leu Glu Glu Val Lys
210          215          220
Asn Leu Ile Leu Glu Ser Asp Leu Tyr Ile Gly Gly Asp Ser Phe Leu
225          230          235          240
Ile His Leu Ala Tyr Tyr Leu Lys Lys Asn Tyr Phe Ile Phe Phe Tyr
245          250          255
Arg Asp Asn Asp Asp Phe Met Pro Pro Asn Ser Gly Asn Glu Asn Phe
260          265          270
Leu Lys Ala His Lys Ser His Phe Ile Glu Gln Asp Leu Ala Lys Lys
275          280          285
Phe Arg His Leu Gly Leu Leu
290          295

```

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588

```

Asn Thr Gln Arg Gln Thr Leu Pro Leu Val Lys Ser Arg Pro His Pro
1           5           10           15
Leu Val Lys Ile Tyr Leu Lys Gln Met Cys Gly Met Gly Phe Ile Gly
20           25           30
Phe Lys Thr Lys Leu Thr Gln Thr Lys Ala Phe Ile Ile Leu Ile Pro
35           40           45

```

SUBSTITUTE SHEET (RULE 26)

1139

Ile Phe Gln Asp Arg Ala Val Lys Ala Ala Thr Arg Ser Ala Pro Ile
 50 55 60
 Gln Leu Ile Cys
 65

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589

Thr Leu Ile Ser Ile Phe Ser Ala Ser Gln Ala Asp Phe Gly Gly Asn
 1 5 10 15
 Thr Thr Ile Asp Thr Ala Ser Phe Asn Phe Asp Ser Ala Ser Ser Leu
 20 25 30
 Asn Phe Asn Asn Leu Thr Ala Asn Gly Ala Leu Asn Phe Asn Gly Tyr
 35 40 45
 Ala Pro Ser Leu Thr Lys Ala Leu Met Asn Val Ser Gly Gln Phe Val
 50 55 60
 Leu Gly Asn Asn Gly Asp Ile Asn Leu Ser Asp Ile Asn Ile Phe Asp
 65 70 75 80
 Asn Ile Thr Lys Ser Val Thr Tyr Asn Ile Leu Asn Ala Gln Lys Gly
 85 90 95
 Ile Thr Gly Ile Ser Gly Ala Asn Gly Tyr Glu Lys Ile Leu Phe Tyr
 100 105 110
 Gly Met Lys Ile Gln Asn Ala Thr Tyr Ser Asp Asn Asn Ile Gln
 115 120 125
 Thr Trp Ser Phe Ile Asn Pro Leu Asn Ser Ser Gln Ile Ile Gln Glu
 130 135 140
 Ser Ile Lys Asn Gly Asp Leu Thr Ile Glu Val Leu Asn Asn Pro Asn
 145 150 155 160
 Ser Ala Ser Asn Thr Ile Phe Asn Ile Ala Pro Glu Leu Tyr Asn Tyr
 165 170 175
 Gln Asp Ser Lys Gln Asn Pro Thr Gly Tyr Ser Tyr Asp Tyr Ser Asp
 180 185 190
 Asn Gln Ala Gly Thr Tyr Tyr Leu Thr Ser Asn Ile Lys Gly Leu Phe
 195 200 205
 Thr Pro Lys Gly Ser Gln Thr Pro Gln Thr Pro Gly Thr Tyr Ser Pro
 210 215 220
 Phe Asn Gln Pro Leu Asn Ser Leu Asn Ile Tyr Asn Lys Gly Phe Ser
 225 230 235 240
 Ser Glu Asn Leu Lys Thr Leu Leu Gly Ile Leu Ser Gln Asn Ser Ala
 245 250 255
 Thr Leu Lys Glu Met Ile Glu Ser Asn Gln Leu Asp Asn Ile Thr Asn
 260 265 270
 Ile Asn Glu Val Leu Gln Leu Leu Asp Lys Ile Lys Ile Thr Gln Ala
 275 280 285
 Gln Lys Gln Ala Leu Leu Glu Thr Ile Asn His Leu Thr Asp Asn Ile
 290 295 300
 Asn Gln Thr Phe Asn Asn Gly Asn Leu Val Ile Gly Ala Thr Gln Asp

SUBSTITUTE SHEET (RULE 26)

1140

| | | | | | | |
|---|---|-----|-----|-----|-----|-----|
| 305 | | 310 | | 315 | | 320 |
| Asn Val Thr Asn Ser | Thr Ser Ser Ile Trp Phe Gly Gly Asn Gly Tyr | | | | | |
| | 325 | | 330 | | 335 | |
| Ser Ser Pro Cys Ala Leu Asp Ser Ala Thr Cys Ser Ser Phe Arg Asn | | | | | | |
| | 340 | | 345 | | 350 | |
| Thr Tyr Leu Gly Gln Leu Leu Gly Ser Thr Ser Pro Tyr Leu Gly Tyr | | | | | | |
| | 355 | | 360 | | 365 | |
| Ile Asn Ala Asp Phe Lys Ala Lys Ser Ile Tyr Ile Thr Gly Thr Ile | | | | | | |
| | 370 | | 375 | | 380 | |
| Gly Ser Ser Asn Ala Phe Glu Ser Gly Gly Ser Ala Asp Val Thr Phe | | | | | | |
| | 385 | | 390 | | 395 | |
| Gln Ser Ala Asn Asn Leu Val Leu Asn Lys Ala Asn Ile Glu Ala Gln | | | | | | |
| | 405 | | 410 | | 415 | |
| Ala Thr Asp Asn Ile Phe Asn Leu Leu Gly Gln Glu Gly Ile Asp Lys | | | | | | |
| | 420 | | 425 | | 430 | |
| Ile Phe Asn Gln Gly Asn Leu Ala Asn Val Leu Ser Gln Met Ala Met | | | | | | |
| | 435 | | 440 | | 445 | |
| Glu Lys Ile Lys Gln Ala Gly Gly Leu Gly Asn Phe Ile Glu Asn Ala | | | | | | |
| | 450 | | 455 | | 460 | |
| Leu Ser Pro Leu Ser Lys Glu Leu Pro Ala Ser Leu Gln Asp Glu Thr | | | | | | |
| | 465 | | 470 | | 475 | |
| Leu Gly Gln Leu Ile Gly Gln Asn Asn Leu Asp Asp Leu Leu Asn Asn | | | | | | |
| | 485 | | 490 | | 495 | |
| Ser Gly Val Met Asn Glu Ile Gln Asn Ile Ile Ser Gln Lys Leu Ser | | | | | | |
| | 500 | | 505 | | 510 | |
| Ile Phe Gly Asn Phe Val Thr Pro Ser Ile Ile Glu Asn Tyr Leu Ala | | | | | | |
| | 515 | | 520 | | 525 | |
| Lys Gln Ser Leu Lys Ser Met Leu Asp Asp Lys Gly Leu Leu Asn Phe | | | | | | |
| | 530 | | 535 | | 540 | |
| Ile Gly Gly Tyr Ile Asp Ala Ser Glu Leu Ser Ser Ile Leu Gly Val | | | | | | |
| | 545 | | 550 | | 555 | |
| Ile Leu Lys Asp Ile Thr Asn Pro Pro Thr Ser Leu Gln Lys Asp Ile | | | | | | |
| | 565 | | 570 | | 575 | |
| Gly Val Val Ala Asn Asp Leu Leu Asn Glu Phe Leu Gly Gln Asp Val | | | | | | |
| | 580 | | 585 | | 590 | |
| Val Lys Lys Leu Glu Ser Gln Gly Leu Val Ser Asn Ile Ile Asn Asn | | | | | | |
| | 595 | | 600 | | 605 | |
| Val Ile Ser Gln Gly Gly Leu Ser Gly Val Tyr Asn Gln Gly Leu Gly | | | | | | |
| | 610 | | 615 | | 620 | |
| Ser Val Leu Pro Pro Ser Leu Gln Asn Ala Leu Lys Glu Asn Asp Leu | | | | | | |
| | 625 | | 630 | | 635 | |
| Gly Thr Leu Leu Ser Pro Arg Gly Leu His Asp Phe Trp Gln Lys Gly | | | | | | |
| | 645 | | 650 | | 655 | |
| Tyr Phe Asn Phe Leu Ser Asn Gly Tyr Val Phe Val Asn Asn Ser Ser | | | | | | |
| | 660 | | 665 | | 670 | |
| Phe Ser Asn Ala Thr Gly Gly Ser Leu Asn Phe Val Ala Asn Lys Ser | | | | | | |
| | 675 | | 680 | | 685 | |
| Ile Ile Phe Asn Gly Asp Asn Thr Ile Asp Phe Ser Lys Tyr Gln Gly | | | | | | |
| | 690 | | 695 | | 700 | |
| Ala Leu Ile Phe Ala Ser Asn Gly Val Ser Asn Ile Asn Ile Thr Thr | | | | | | |
| | 705 | | 710 | | 715 | |
| Leu Asn Ala Thr Asn Gly Leu Ser Leu Asn Ala Gly Leu Asn Asn Val | | | | | | |
| | 725 | | 730 | | 735 | |
| Ser Val Gln Lys Gly Glu Ile Cys Ile Asn Leu Ala Asn Cys Pro Thr | | | | | | |
| | 740 | | 745 | | 750 | |
| Thr Lys Asn Ser Ser Pro Ala Asn Ser Ser Val Thr Pro Thr Asn Glu | | | | | | |
| | 755 | | 760 | | 765 | |
| Ser Leu Ser Val His Ala Asn Asn Phe Thr Phe Leu Gly Thr Ile Ile | | | | | | |
| | 770 | | 775 | | 780 | |
| Ser Asn Gly Ala Ile Asp Leu Ser Gln Val Thr Asn Asn Ser Val Ile | | | | | | |
| | 785 | | 790 | | 795 | |
| Gly Thr Leu Asn Leu Asn Glu Asn Ala Thr Leu Gln Ala Asn Asn Leu | | | | | | |
| | 805 | | 810 | | 815 | |
| Thr Ile Thr Asn Ala Phe Asn Asn Ala Ser Asn Ser Thr Ala Asn Ile | | | | | | |
| | 820 | | 825 | | 830 | |

SUBSTITUTE SHEET (RULE 26)

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Asp Gly Asn Phe Thr Leu Asn Gln Gln Ala Thr Leu Ser Thr Asn Ala
 835 840 845
 Ser Gly Leu Asn Val Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val
 850 855 860
 Phe Asn Leu Ser His Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly
 865 870 875 880
 Thr Ala Thr Ile Met Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala
 885 890 895
 Ser Ser Pro Glu Val Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala
 900 905 910
 Ile Tyr Tyr Gly Tyr Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp
 915 920 925
 Asn Tyr Leu Lys Leu Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met
 930 935 940
 Val Met Thr Asp Asn Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val
 945 950 955 960
 Lys Asp Gly Gly Leu Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr
 965 970 975
 Ile Tyr Thr Ser Ile Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn
 980 985 990
 Asp Pro Ile Asn Asn Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala
 995 1000 1005
 Gln Ile Gln Gly Val Gln Ser Val Asp Ser Ile Asp Gln Ala Gly Gly
 1010 1015 1020
 Asn Gln Ala Ile Asn Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser
 1025 1030 1035 1040
 Pro Leu Phe Ala Pro Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu
 1045 1050 1055
 Thr Thr Ile Ala Gly Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn
 1060 1065 1070
 Pro Asn Phe Lys Asn Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr
 1075 1080 1085
 Thr Gln Gln Met Ser Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe
 1090 1095 1100
 Ala Arg Ser Asp Phe Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg
 1105 1110 1115 1120
 Phe Ala Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser
 1125 1130 1135
 Gln Arg Asn Arg Val Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly
 1140 1145 1150
 Ala Ser Phe Ile Ser Gly Gly Thr Gly Thr Leu Tyr Gly Ile Asn Val
 1155 1160 1165
 Gly Tyr Asp Arg Phe Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala
 1170 1175 1180
 Tyr Gly Tyr Ser Gly Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser
 1185 1190 1195 1200
 Asn Val Asn Val Gly Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu
 1205 1210 1215
 Leu Thr Met Ser Leu Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile
 1220 1225 1230
 Asn Ser Tyr Asp Pro Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr
 1235 1240 1245
 Asp Thr Trp Thr Thr Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met
 1250 1255 1260
 Phe Lys Asp Lys Ser Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr
 1265 1270 1275 1280
 Tyr Tyr Ile Gly Leu Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile
 1285 1290 1295
 Tyr Asn Gln Phe Arg Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu
 1300 1305 1310
 Thr Ile Asn Phe Ala Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser
 1315 1320 1325
 Tyr Tyr Phe Val Ile Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser
 1330 1335 1340
 Met Gly Asp Lys Met Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr

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1142

1345 1350 1355 1360
 Arg Asp Gly Gly Arg Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly
 1365 1370 1375
 Glu Ile Arg Leu Phe Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala
 1380 1385 1390
 Arg Phe Gly Leu Asp Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly
 1395 1400 1405
 Met Arg Tyr Ala Phe
 1410

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590

Arg Asp Asn Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala
 1 5 10 15
 Asn Leu Leu Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr
 20 25 30
 Phe Asp Glu Ser Leu Lys Thr Thr Asp Pro Arg Glu Phe Val Tyr
 35 40 45
 Leu Ala Cys Lys Gly Lys Leu Glu Lys Ala Lys Glu Leu Leu Ala Asn
 50 55 60
 Asn Cys Ala Ile Val Val Ala Asp Ser Val Val Ser Val Gly Asn Arg
 65 70 75 80
 Met Gln Arg Lys Ala Lys Asn Lys Arg Glu Ala Leu Glu Phe Leu Lys
 85 90 95
 Arg Gln Asn Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile
 100 105 110
 Ser Pro Val Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu
 115 120 125
 Lys Ala Phe Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu
 130 135 140
 Trp Gln Gly Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro
 145 150 155 160
 Tyr Ile Lys Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn
 165 170 175
 Val Glu Gly Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu
 180 185 190
 Leu

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591

```

Arg Met Ala Leu Phe Gly Ser Lys Ser Lys Met Leu Glu Thr Tyr Ala
1      5      10      15
Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu Pro Lys
20     25     30
Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala Lys Pro
35     40     45
Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val Gly Tyr
50     55     60
Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile His Ala
65     70     75     80
Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His Asp Phe
85     90     95
Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu Arg Gln
100    105    110
Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu Leu Ala
115    120    125
His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile Thr Gln
130    135    140
Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn Leu Leu
145    150    155    160
Ser Phe Lys Thr Leu Tyr Pro Phe
165

```

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592

```

Asn Asp Asp Glu Asn Lys Val Ile Glu Leu Lys Thr Arg Asn Asn Met
1      5      10      15
Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu Arg
20     25     30
Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu Phe
35     40     45
Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala Pro

```

SUBSTITUTE SHEET (RULE 26)

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| | | | | | |
|-------------------------|---------------------|-----------------|---------|----|--|
| 50 | | 55 | | 60 | |
| Glu Thr Lys Thr Tyr Ile | Leu Glu Asn His | Leu Asn Ile Pro | Ile Phe | | |
| 65 | 70 | 75 | 80 | | |
| Gln Pro Gln Ser Leu Lys | Glu Pro Glu Val Gln | Ile Leu Lys Gly | Leu | | |
| | 85 | 90 | 95 | | |
| Lys Pro Asp Phe Ile Val | Val Val Ala Tyr Gly | Lys Ile Leu Pro | Lys | | |
| | 100 | 105 | 110 | | |
| Glu Val Leu Thr Ile Ala | Pro Cys Ile Asn Leu | His Ala Ser Leu | Leu | | |
| | 115 | 120 | 125 | | |
| Pro Lys Tyr Arg Gly Ala | Ser Pro Ile His Glu | Met Ile Leu Asn | Asp | | |
| | 130 | 135 | 140 | | |
| Asp Arg Ile Tyr Gly Ile | Ser Thr Met Leu Met | Asp Leu Glu Leu | Asp | | |
| 145 | 150 | 155 | 160 | | |
| Ser Gly Asp Ile Leu Glu | Ser Ala Ser Phe Leu | Arg Glu Asp Tyr | Leu | | |
| | 165 | 170 | 175 | | |
| Asp Leu Asp Ala Leu Ser | Leu Lys Leu Ala Arg | Met Gly Ala Thr | Leu | | |
| | 180 | 185 | 190 | | |
| Leu Leu Ser Thr Leu Lys | Asn Phe His Ser Ile | Thr Arg Lys Pro | Gln | | |
| | 195 | 200 | 205 | | |
| Asp His Met Gln Ala Ser | Phe Cys Lys Lys Ile | Ala Lys Ala Asp | Gly | | |
| | 210 | 215 | 220 | | |
| Leu Val Gly Phe Lys Asp | Ala Lys Asn Leu Phe | Leu Lys Ser Leu | Ala | | |
| 225 | 230 | 235 | 240 | | |
| Phe Lys Ser Trp Pro Glu | Ile Phe Leu Glu Asn | Ser Leu Lys Leu | Leu | | |
| | 245 | 250 | 255 | | |
| Glu Val Glu Leu Val Glu | Asn Glu Lys Ser His | Lys Glu Gly Glu | Ile | | |
| | 260 | 265 | 270 | | |
| Leu Ala Ile Asp Glu Arg | Gly Val Leu Val Gly | Cys Leu Lys Gly | Ser | | |
| | 275 | 280 | 285 | | |
| Val Arg Ile Ala Arg Leu | Gln Ala Val Gly Lys | Lys Pro Leu Lys | Ala | | |
| | 290 | 295 | 300 | | |
| Lys Asp Tyr Leu Asn Gly | Arg Arg Leu Lys Val | Gly Gly Ile Leu | Thr | | |
| 305 | 310 | 315 | 320 | | |

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593

| | | |
|-------------------------|---------------------|---------------------|
| Lys Ser Thr Arg Lys Thr | Ile Met Glu Ala Gln | Leu Arg Phe Thr Gly |
| 1 | 5 | 10 |
| Val Gly Gly Gln Gly Val | Leu Leu Ala Gly Glu | Ile Leu Ala Glu Ala |
| | 20 | 25 |
| Lys Ile Val Ser Gly Gly | Tyr Gly Thr Lys Thr | Ser Thr Tyr Thr Ser |
| | 35 | 40 |
| Gln Val Arg Gly Gly Pro | Thr Lys Val Asp Ile | Leu Leu Asp Lys Asp |
| | 50 | 55 |
| Glu Ile Ile Phe Pro Tyr | Ala Lys Glu Gly Glu | Ile Asp Phe Met Leu |
| 65 | 70 | 75 |

SUBSTITUTE SHEET (RULE 26)

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```

Ser Val Ala Gln Ile Ser Tyr Asn Gln Phe Lys Ser Asp Ile Lys Lys
      85          90          95
Gly Gly Ile Val Val Ile Asp Pro Asn Leu Val Thr Pro Thr Lys Glu
      100        105        110
Asp Glu Glu Lys Tyr Gln Leu Tyr Lys Ile Pro Ile Ile Ser Ile Ala
      115        120        125
Lys Asp Glu Val Gly Asn Ile Ile Thr Gln Ser Val Val Ala Leu Ala
      130        135        140
Ile Thr Val Glu Leu Thr Lys Cys Val Glu Glu Asn Ile Val Leu Asp
145          150          155          160
Thr Met Leu Lys Lys Val Pro Cys Lys Ser Arg
      165          170

```

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594

```

Ala Cys Leu Lys Gln Glu Asn Ile Thr Asn Thr Gln Ile Leu His Ile
1      5      10      15
Gly Asp Asn Ser Trp Ala Asp Asp Ala Met Pro Lys Ser Leu Gly Ile
      20      25      30
Ala Thr Leu Phe Arg Lys Ser Val Leu Lys Gln Leu Glu Val Phe
      35      40      45
Pro Lys Tyr Lys Thr Phe Asn Pro Thr Ser Val Ala Gln Ser Phe Ile
      50      55      60
Leu Gly Ser Leu Cys Val Phe Tyr Lys Asn Tyr Ile Gln Lys His Glu
      65      70      75      80
Lys Phe Asp Tyr Trp Phe Leu Leu Gly Ala Met Gln Ala Gly Ile Ala
      85      90      95
Ala Val Ala Tyr Cys Gln Phe Ile Tyr Lys Glu Ile His Lys Arg Asn
      100     105     110
Ile Asp Thr Leu Val Phe Val Ala Arg Asp Gly Tyr Leu Leu Gln Lys
      115     120     125
Ile Phe Asn Ile Leu Tyr Pro Asn Ser Tyr Lys Thr Thr Tyr Val Tyr
      130     135     140
Ala Pro Arg Ile Leu Lys Lys Ala Val Phe Leu Glu Val Val Glu Gly
145     150     155     160
Glu Ser Leu Glu Ile Leu Arg Ile Leu Glu Gly Glu Glu Val Lys
      165     170     175
Lys Lys Gln Ile Thr Thr Asn Gln Gln Ala Tyr Val Tyr Leu Tyr Ser
      180     185     190
Asn Phe Glu His Cys Arg His Leu Ala Leu Lys Cys Leu Asp Asn Tyr
      195     200     205
Arg Lys Tyr Leu Phe Ser Ser Asn Leu Glu Gly Asn Ile Ala Ile Val
      210     215     220
Asp Thr Ile Thr Leu Gly Tyr Ser Ser Gln Gly Leu Ile Gln Lys Ala
225     230     235     240
Leu Asn Lys Glu Val Phe Gly Cys Tyr Val Asp Leu Leu Arg Ile Leu

```

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```

                245                250                255
Asn Tyr Asp Cys Val Ser Phe Leu Pro Phe Ser His Pro Lys Pro Val
      260      265      270
Tyr Phe His Asn Trp Asp Phe Met Glu Phe Leu Leu Thr Ser Pro Glu
      275      280      285
Tyr Pro Ile Leu Asn Val Glu Asn Gly Val Pro Ile Tyr Gln Lys Asp
      290      295      300
Val Ser Ser Cys Glu Lys His Arg Ser Lys Ala Tyr Glu Lys Ile Val
      305      310      315      320
Glu Gly Ala Val Gly Tyr Ala Ser Tyr Phe Lys Glu Ser Gln Ile Ser
      325      330      335
Leu Asp Ile His Asp Val Ile Glu Trp Val Asn Phe Phe Ile Asp Asn
      340      345      350
Pro Ser Ile Gln Asp Gln Glu Gln Phe Arg Gln Ile Tyr Phe Leu Pro
      355      360      365
Asp Ala Thr His Lys Asn Ala Leu Pro Leu Phe Cys Asn Asp Val Ser
      370      375      380
Leu Leu Ser Cys Ile Leu Lys Pro Ser Gln Ser Tyr Ser Val Leu Lys
      385      390      395      400
Arg Ser Leu Arg Thr Asn Lys Gln Glu Arg Leu Phe Lys Ile Leu Ser
      405      410      415
Leu Ile Lys Lys Ile Tyr Gly Lys Leu Lys Lys Lys
      420      425

```

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595

```

Gly Leu Leu Ala Cys Leu Leu Val Leu Leu Asn Leu Lys Ile Thr Pro
1      5      10      15
Asn Leu Met Trp Pro Leu Asp Ile Ile Val Val Val Ala Trp Val Leu
      20      25      30
Trp Gly Val Asn Met Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr
      35      40      45
Ile Tyr Val Ser Leu Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala
      50      55      60
Val Met Tyr Ile Phe Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala
      65      70      75      80
Asp Met Gly Ser Val Trp His Ser Ile Ser Met Tyr Ser Gly Ser Asn
      85      90      95
Asp Ala Leu Ile Gln Trp Trp Trp Gly His Asn Ala Val Ala Phe Val
      100      105      110
Phe Thr Ser Gly Val Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu
      115      120      125
Ser Gly Gln Pro Ile Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp
      130      135      140
Ser Leu Met Phe Val Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr
      145      150      155      160

```

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Ser Thr Val Pro Asp Trp Val Gln Thr Leu Ser Ser Val Phe Ser Val
 165 170 175
 Val Leu Ile Leu Pro Ser Trp Gly Thr Ala Ile Asn Met Leu Leu Thr
 180 185 190
 Met Arg Gly Gln Trp His Gln Leu Lys Glu Ser Pro Leu Ile Lys Phe
 195 200 205
 Leu Val Leu Ala Ser Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser
 210 215 220
 Ile Gln Ala Ile Lys Ser Val Asn Ala Leu Ala His Phe Thr Asp Trp
 225 230 235 240
 Ile Ile Gly His Val His Asp Gly Val Leu Gly Trp Val Gly Phe Thr
 245 250 255
 Leu Ile Ala Ser Met Tyr His Met Thr Pro Arg Leu Phe Lys Arg Glu
 260 265 270
 Ile Tyr Ser Gly Arg Leu Val Asp Phe Gln Phe Trp Ile Met Thr Leu
 275 280 285
 Gly Ile Val Leu Tyr Phe Ser Ser Met Trp Ile Ala Gly Ile Thr Gln
 290 295 300
 Gly Met Met Trp Arg Asp Val Asp Gln Tyr Gly Asn Leu Thr Tyr Gln
 305 310 315 320
 Phe Ile Asp Thr Val Lys Ala Leu Ile Pro Tyr Tyr Asn Ile Arg Gly
 325 330 335
 Val Gly Gly Leu Met Tyr Phe Ile Gly Phe Ile Ile Phe Ala Tyr Asn
 340 345 350
 Ile Phe Met Thr Ile Thr Ala Gly Lys Lys Leu Glu Arg Glu Pro Asn
 355 360 365
 Tyr Ala Thr Pro Met Ala Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596

Gly Phe Asp Asp Asp Met Glu Ile Arg Asn Ile Lys Glu Phe Glu Lys
 1 5 10 15
 Ala Ser Lys Lys Leu Gln Lys Asp Thr Leu Lys Ile Ala Leu Ala Leu
 20 25 30
 Leu Phe Leu Ile Gly Ala Ala Leu Leu Ala Leu Ile Phe Gly Gln Ala
 35 40 45
 Asn Ser Lys Gly Leu Leu Leu Ile Phe Ala Ala Val Ile Gly Gly Tyr
 50 55 60
 Met Ala Met Asn Ile Gly Ala Asn Asp Val Ser Asn Asn Val Gly Pro
 65 70 75 80
 Ser Val Gly Ser Lys Ala Ile Ser Met Gly Gly Ala Ile Leu Ile Ala
 85 90 95
 Ala Val Cys Glu Met Leu Gly Ala Ile Ile Ala Gly Gly Glu Val Val
 100 105 110
 Ser Thr Ile Lys Gly Arg Ile Val Ser Pro Glu Phe Ile Asn Asp Ala

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```

      115      120      125
His Val Phe Ile Asn Val Met Leu Ala Ser Leu Leu Ser Gly Ala Leu
      130      135      140
Trp Leu His Val Ala Thr Leu Ile Gly Ala Pro Val Ser Thr Ser His
      145      150      155      160
Ser Val Val Gly Gly Ile Met Gly Ala Gly Met Ala Ala Ala Gly Met
      165      170      175
Ser Ala Ile Asn Trp His Phe Leu Ser Gly Ile Val Ala Ser Trp Val
      180      185      190
Ile Ser Pro Leu Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu
      195      200      205
Ile Lys Lys Thr Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu
      210      215      220
Lys Val Val Pro Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp
      225      230      235      240
Tyr Leu Ile Val Lys Val Leu Lys Arg Leu Tyr Ala Val Gly Phe Glu
      245      250      255
Ile Gln Leu Ala Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu
      260      265      270
Phe Lys Arg Phe Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His
      275      280      285
Glu Ser Val Asn Glu Leu Phe Asn Val Pro Leu Ile Phe
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597

```

Arg Met Lys Leu Lys Lys Thr Leu Thr Tyr Gln His His Ala Tyr Ser
1      5      10      15
Phe Leu Ser Asp Asn Thr Asn Glu Val Leu Glu Asn Pro Lys Glu Ile
      20      25      30
Leu Phe Val Lys Thr Pro Leu Asn Glu Lys Tyr Ala Pro Leu Ile Ala
      35      40      45
Glu Lys Asn Leu Ala Ile Leu Asp Phe Asn Glu Leu Lys Asn Tyr Phe
      50      55      60
Asp Phe Lys Ile Lys Ile Val Gly Ile Thr Gly Thr Asn Gly Lys Thr
      65      70      75      80
Thr Thr Ala Ser Leu Met Tyr Ser Leu Leu Asp Leu Asn Lys Lys
      85      90      95
Thr Ala Leu Leu Gly Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile
      100      105      110
Lys Glu Lys Gly Leu Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp
      115      120      125
Leu Glu Glu Ala Ile Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val
      130      135      140
Ser Ser His Ala Ile Val Gln Lys Arg Ile Ala Gly Leu Asp Phe Ala
      145      150      155      160

```

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Leu Lys Ile Leu Thr Asn Ile Thr Ser Asp His Leu Asp Phe His Gln
 165 170 175
 Asn Ile Glu Asn Tyr Arg Asp Ala Lys Asn Ser Phe Phe Lys Asp Glu
 180 185 190
 Gly Leu Lys Val Ile Asn Arg Asp Glu Thr Asn Ala Leu Phe Asn Pro
 195 200 205
 Ile Asn Ala Arg Thr Tyr Ala Leu Asp Lys Lys Ala His Leu Asn Val
 210 215 220
 Gln Ala Phe Ser Leu Asn Pro Ser Ile Ser Ala Ser Leu Cys Tyr Gln
 225 230 235 240
 His Asp Leu Arg Asp Pro Asn Leu Lys Glu Thr Ala Leu Ile His Ser
 245 250 255
 Pro Leu Leu Gly Arg Tyr Asn Leu Tyr Asn Ile Leu Ala Gly Val Leu
 260 265 270
 Gly Val Lys Leu Leu Thr Gln Leu Pro Leu Glu Thr Ile Ala Pro Leu
 275 280 285
 Leu Glu Asn Phe Tyr Gly Val Lys Gly Arg Leu Glu Ile Val His Ser
 290 295 300
 Lys Pro Leu Val Val Val Asp Phe Ala His Thr Thr Asp Gly Met Gln
 305 310 315 320
 Gln Val Phe Glu Ser Phe Lys Asn Gln Lys Ile Thr Ala Leu Phe Gly
 325 330 335
 Ala Gly Gly Asp Arg Asp Lys Thr Lys Arg Pro Lys Met Gly Ala Ile
 340 345 350
 Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser Asp Asn Pro Arg
 355 360 365
 Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu Lys Gly Ile Asn
 370 375 380
 Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys Lys Ala Ile Leu
 385 390 395 400
 Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu Leu Ile Leu Gly
 405 410 415
 Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys Thr Ile Phe Phe
 420 425 430

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598

Arg Leu Leu Ser Gln Phe Lys Thr Arg Ile Asn Met Gln Glu Phe Ser
 1 5 10 15
 Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn Asp Phe Leu
 20 25 30
 Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser Asn Pro Ser
 35 40 45
 Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Gln Asp Glu Ile
 50 55 60
 Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu Thr Leu Ala

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```

65          70          75          80
Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro Leu Tyr Glu
85          90          95
Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp Pro Phe Leu
100        105        110
Glu Asp Asp Ala Ile Lys Ser Ile Asp Glu Ala Lys Arg Leu Phe Lys
115        120        125
Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala Ser Glu Ser
130        135        140
Ala Phe Glu Val Ile Ser Ala Leu Ala Gln Ala Ser Ile Pro Ile Asn
145        150        155        160
Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile Ala Gln Ile
165        170        175
Leu Ala Lys Glu Ala Arg Lys Arg Ala Val Ile Ser Val Phe Val Ser
180        185        190
Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Gln Asn Leu Gln Ala
195        200        205
Gln Ser Gly Ile Met Asn Ala Thr Glu Cys Tyr Tyr Gln Ile Asn Gln
210        215        220
His Ala Asn Lys Leu Ile Ser Thr Leu Phe Ala Ser Thr Gly Val Lys
225        230        235        240
Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu Cys Phe Lys
245        250        255
Asn Ser Ile Asn Thr Ala Pro Leu Asp Ala Leu Asn Ala Tyr Leu Leu
260        265        270
Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Ile Thr Glu Ile Glu
275        280        285
Ala Phe Lys Lys Glu Leu Lys Thr His Asn Ile Asp Leu Glu Asn Thr
290        295        300
Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala Phe Lys Gln Ser Phe
305        310        315        320
Glu Lys Leu Leu Ser Ser Phe
325

```

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599

```

Gly Phe Lys Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys
1          5          10          15
Tyr Phe Leu Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile
20        25        30
Asp Ser Leu Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile
35        40        45
Ile Leu Phe Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu
50        55        60
Pro Ile Ser Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile
65        70        75        80

```

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```

Lys Ser Asn Gln Tyr Thr Ala Leu Leu Ser Ile Gly Phe Ser Lys Cys
      85          90          95
Gln Ile Leu Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val
      100        105        110
Tyr Val Gly Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr
      115        120        125
Gln Asn Leu Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Glu His Leu
      130        135        140
Leu Val Lys Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro
      145        150        155        160
Leu Leu Gln Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys
      165        170        175
Thr Leu Glu Ser Tyr Ala Glu Ala Lys Glu Ala Phe Phe Glu Asp Lys
      180        185        190
Tyr Trp Ile Leu His Asp Thr Thr Ile Tyr Glu Met Pro Leu Ser Phe
      195        200        205
Glu Leu Gly Ala Asn Ala Leu Asn Thr Thr His Leu Glu Thr Phe Lys
      210        215        220
Thr Leu Lys Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn
      225        230        235        240
Lys Pro Ala Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu
      245        250        255
Val Arg Gln Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val
      260        265        270
Phe Ala Ile Leu Pro Phe Phe Val Pro Phe Leu Ser Val Leu Ile Ala
      275        280        285
Tyr Phe Ser Pro Ser Leu Ala Arg Tyr Glu Asn Leu Ala Leu Leu Gly
      290        295        300
Leu Lys Phe Ile Ile Ile Thr Leu Val Val Trp Gly Leu Phe Phe Ala
      305        310        315        320
Leu Gly Lys Phe Ser Ile Ser Gly Ile Leu Ile Pro Glu Ile Gly Val
      325        330        335
Leu Ser Pro Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys
      340        345        350
Lys Leu Asn Lys Arg Leu
      355

```

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600

```

Lys Arg Arg Val Val Lys Phe Tyr Thr Tyr Ser Gly Glu Thr Ala Ala
1      5          10          15
Glu Ala Leu Lys Ile Ala Gln Ser His Gly Val Asp Thr Leu Val
      20        25        30
Phe Lys Thr Gln Glu Ile Arg Lys Lys Thr Leu Thr Ser Ser Gly Leu
      35        40        45
Tyr Glu Ile Val Val Ala Val Glu Glu Glu Glu Asn Lys Lys Ala Pro

```

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```

      50      55      60
Leu Ile Pro Glu Ser Leu Tyr Asp Glu Glu Leu Asn Glu Glu Asp Val
65      70      75      80
Val Met Gln Leu Ser Ser Thr Val Glu Glu Met Arg Lys Leu Ala Gly
      85      90      95
Val Ser Ser Asn Gln Arg Asn Tyr Thr Phe Ser Lys Asn Lys Thr Leu
      100      105      110
Leu Glu Lys Asp Ala Pro Leu Glu Asp Thr Pro Leu Glu Ala Asn Lys
      115      120      125
Gln Asp Ala Leu Leu Gln Ala Leu Lys Asp Glu Ala Asn His Lys Lys
      130      135      140
Glu Arg Glu Lys Arg Glu Val Lys Gln Glu Glu Ile Lys Asp Ile
145      150      155      160
Asn Ala Gln Leu Ser Lys Ile Arg Asp Ser Leu Lys Leu Ile Gln Asn
      165      170      175
Met Phe Trp Asp Glu Lys Asn Pro Asn Ser Val Asn Ile Pro Gln Glu
      180      185      190
Phe Ala Glu Ile Tyr Lys Leu Ala Lys Gln Ser Gly Met Lys Ser Ser
      195      200      205
His Leu Asp Glu Ile Met Gln Leu Ser Leu Glu Leu Met Pro Leu Arg
      210      215      220
Met Arg Glu Asn Ser Val Thr Ile Lys Arg Tyr Phe Arg Glu Val Leu
      225      230      235      240
Arg Lys Ile Ile Leu Cys Arg Pro Glu Asp Leu Asn Leu Arg Gln Lys
      245      250      255
Arg Ile Leu Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr
      260      265      270
Leu Ala Lys Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr
      275      280      285
Lys Val Gly Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu
      290      295      300
Gln Leu Ser Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val
      305      310      315      320
Ile Asp Ala Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys
      325      330      335
Asp Phe Ile Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu
      340      345      350
Lys Ile Ala Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp
      355      360      365
Val Ser Leu Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp
      370      375      380
Ile Tyr Asp Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr
      385      390      395      400
Lys Leu Asp Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His
      405      410      415
Glu Ser Gln Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro
      420      425      430
Met Asp Leu Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu
      435      440      445
Asp Gly Phe Ser Asn Pro Asn Lys Glu Gln Ala
      450      455

```

(2) INFORMATION FOR SEQ ID NO:1601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601

```

Ile Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu
1      5      10      15
Val Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile
20      25      30
Ile Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg
35      40      45
Val Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met
50      55      60
Ala Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val
65      70      75      80
Glu Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu
85      90      95
Met Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro
100     105     110
Met Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro
115     120     125
Met Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn
130     135     140
Arg Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg
145     150     155     160
Gln Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met
165     170     175
Tyr Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile
180     185     190
Val Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile
195     200     205
Gly His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile
210     215     220
Glu Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu
225     230     235     240
Thr Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser
245     250     255
Gly Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser
260     265     270
Leu Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn
275     280     285
Lys Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg
290     295     300
Tyr Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile
305     310     315     320
Lys Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu
325     330     335
Met Leu Glu Glu Gln Arg Arg Gly Lys Val Gly Asp Ile Met Lys Ile
340     345     350
Glu Glu Glu
355

```

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602

```

Gly Thr Ser Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn
1      5      10      15
Ala Lys Asn Pro Lys Ser Phe Phe Asp Asn Lys Gly Asn Thr Lys Phe
20      25      30
Ile Ala Ile Thr Ser Gly Lys Gly Val Gly Lys Ser Asn Ile Ser
35      40      45
Ala Asn Leu Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val
50      55      60
Phe Asp Ala Asp Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val
65      70      75      80
Lys Thr His Lys Asn Ile Leu His Ala Leu Lys Gly Glu Ala Lys Leu
85      90      95
Gln Glu Ile Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly
100     105     110
Asp Ser Gly Glu Glu Ile Leu Lys Tyr Ile Ser Gly Ala Glu Ala Leu
115     120     125
Asp Arg Phe Val Asp Glu Glu Gly Val Leu Ser Ser Leu Asp Tyr Ile
130     135     140
Val Ile Asp Thr Gly Ala Gly Ile Gly Ala Thr Thr Gln Ala Phe Leu
145     150     155     160
Asn Ala Ser Asp Cys Val Val Ile Val Thr Thr Pro Asp Pro Ser Ala
165     170     175
Ile Thr Asp Ala Tyr Ala Cys Ile Lys Ile Asn Ser Lys Asn Lys Asp
180     185     190
Glu Leu Phe Leu Ile Ala Asn Met Val Ala Gln Pro Lys Glu Gly Arg
195     200     205
Ala Thr Tyr Glu Arg Leu Phe Lys Val Ala Lys Asn Asn Ile Ala Ser
210     215     220
Leu Glu Leu His Tyr Leu Gly Ala Ile Glu Asn Ser Ser Leu Leu Lys
225     230     235
Arg Tyr Val Arg Glu Arg Lys Ile Leu Arg Lys Ile Ala Pro Asn Asp
240     245     250     255
Leu Phe Ser Gln Ser Ile Asp Gln Ile Ala Ser Leu Leu Val Ser Lys
260     265     270
Leu Glu Thr Gly Thr Leu Glu Ile Pro Lys Glu Gly Leu Lys Ser Phe
275     280     285
Phe Lys Arg Leu Leu Lys Tyr Leu Gly
290     295

```

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1155

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603

```

Ile Ser Glu Phe Asn His Arg Ser Ala Pro Leu Ile Ile Asn Tyr Val
1      5      10      15
Asn Thr Ile Phe Lys Lys Ala Tyr Gln Asn Ser Pro Thr Ala Tyr Leu
20      25      30
Glu Gln Lys Tyr Pro Lys Thr Ser Asn Asn Lys His Val Thr Glu Gly
35      40      45
Tyr Val Lys Val Ser Leu Val Ala Asp Glu Lys Glu Leu Leu Leu Glu
50      55      60
Gln Ile Leu Gln Glu Ala Gln Asn Leu Leu Glu His Arg Ile Asp Pro
65      70      75      80
Lys Asp Ile Thr Ile Leu Cys Ala Thr Asn Lys Asp Ala Leu Glu Ile
85      90      95
Lys Asn Tyr Leu Gln Glu Tyr Leu Ser Ala Ile Arg Pro Ser Thr Glu
100      105      110
Ser Ser Ala Lys Leu Ser Gln Leu Val Glu Ser Lys Ile Ile Lys Asn
115      120      125
Ala Leu Glu Tyr Ala Leu Ala Glu Glu Pro Tyr Lys Pro Phe Tyr Lys
130      135      140
His Ser Val Leu Lys Leu Ala Gly Tyr Leu His Asp Asp Val Ile Ala
145      150      155      160
Leu Pro Gly Phe Asn Pro Lys Lys Glu Ser Val Ala Ser Phe Val Trp
165      170      175
Lys Ile Met Glu Gln Phe Lys Leu Tyr Glu Glu Pro Ala Gln Ser Cys
180      185      190
Leu Glu Leu Ala Val Gly Cys Glu Asp Ala Asp Gly Phe Leu Glu Lys
195      200      205
Leu Glu Ala Lys Glu Ile Ala Ser Phe Asn Pro Lys Gly Ala Gln Ile
210      215      220
Met Thr Ile His Lys Ser Lys Gly Met Gln Phe Pro Tyr Val Ile Val
225      230      235      240
Cys Glu Arg Leu Gly Asn Pro Asn Ser Ser His Ala Asn Gln Leu Leu
245      250      255
Glu Glu Tyr Asp Gly Thr Glu Leu Ala Arg Leu Tyr Tyr Arg Met Lys
260      265      270
Asn Arg Glu Val Val Asp Lys Asp Tyr Ala Arg Ala Leu Asp Lys Glu
275      280      285
Glu Ala Ala Lys Asp His Glu Glu Ile Asn Val Tyr Tyr Val Ala Phe
290      295      300
Thr Arg Ala Glu Leu Gly Leu Ile Val Val Ala Lys Asp Lys Lys Glu
305      310      315      320
Ser Lys Lys Glu Ser Lys Asn Lys Lys Met His Glu Gln Leu Glu Leu
325      330      335
Ala Pro Leu Glu Glu Gly Glu Ile Ala Pro Val Ile Ser Pro Gln Lys
340      345      350
Glu Pro Leu Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu
355      360      365
Gln Val Gln Glu Ile Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn
370      375      380
Asn Asp Gln Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu
385      390      395      400
Glu Tyr Gln Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr
405      410      415
Leu Asn Tyr His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu
420      425      430
Glu Ser Leu Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe
435      440      445
Lys Asn His Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val
450      455      460
Val Ser Arg Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr

```

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```

465          470          475          480
Val Leu Asp Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala
          485          490          495
Gln Val Ser His Tyr Ala Glu Phe Leu Arg Thr Gln Ala Pro His Phe
          500          505          510
Lys Ile Gln Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys
          515          520          525
Leu Trp Val
          530

```

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604

```

Leu Ser Thr Ala Tyr Gln Ala Val Glu Leu His Trp Phe Leu Lys Ala
1          5          10          15
Val Leu Val Leu Glu Arg Ser Pro Ser Ser Pro Glu Ile Lys Gly Ile
20          25          30
Trp Asp Arg Asp Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp
35          40          45
Val Ser Tyr Asp Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val
50          55          60
Ile Phe Ser Ser Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr
65          70          75          80
Leu Asn Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val
85          90          95
Tyr Gly Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile
100          105          110
Asp Leu Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr
115          120          125
Asn Thr Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly
130          135          140
Val Thr Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp
145          150          155          160
Glu Phe Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr
165          170          175
Glu Leu Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp
180          185          190
Phe Phe Asp Phe Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser
195          200          205
Phe Phe Tyr Asn Ala Pro Thr Thr Ala Asn Phe Lys Asp Tyr Gly
210          215          220
Val Val Gly Ala Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly
225          230          235          240
Leu Gln Ile Glu Trp Ile Ser Pro Met Gly Pro Trp Cys
245          250

```

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(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Ile | Met | Leu | Asp | Lys | Arg | Ile | Lys | Thr | Leu | Leu | Leu | Phe | Phe |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Gly | Leu | Asn | Met | Val | Cys | Leu | Ser | Val | Ser | Phe | Thr | Asn | Lys | Pro | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Cys | Phe | Trp | Phe | Leu | Val | Leu | Gly | Cys | Tyr | Leu | Val | Tyr | Glu | Trp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Lys | Lys | Gln | Lys | Lys | Asp | Phe | Gln | Ser | Ala | Lys | Ser | Leu | Lys | Phe |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| Asp | Ser | Val | Ser | Glu | Leu | Glu | Lys | Asp | Leu | Asn | Met | Glu | Val | Thr | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asp | Glu | Trp | Asp | Thr | His | | | | | | | | | | |
| | | | | | 85 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Ser | Val | Glu | Met | Asn | Tyr | Pro | Asn | Leu | Pro | Asn | Ser | Ala | Leu |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Glu | Ile | Ser | Glu | Gln | Pro | Glu | Val | Lys | Glu | Ile | Thr | Asn | Glu | Leu | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Gln | Leu | Gln | Asn | Ala | Leu | Arg | Ser | Asn | Ala | His | Phe | Ser | Glu | Gln |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Val | Glu | Leu | Ser | Leu | Lys | Cys | Ile | Val | Arg | Ile | Leu | Glu | Val | Leu | Leu |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Ser | Leu | Asp | Phe | Phe | Lys | Asn | Ala | Asn | Glu | Ile | Asp | Ser | Ser | Leu | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asn | Ser | Ile | Glu | Trp | Leu | Thr | Asn | Ala | Gly | Glu | Ser | Leu | Lys | Leu | Lys |

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | | 85 | | | | 90 | | | | 95 | | | | |
| Met | Lys | Glu | Tyr | Glu | Arg | Phe | Phe | Ser | Glu | Phe | Asn | Thr | Ser | Met | His | |
| 100 | | | | | | | | 105 | | | | 110 | | | | |
| Ala | Asn | Glu | Gln | Glu | Val | Thr | Asn | Thr | Leu | Asn | Ala | Asn | Ala | Glu | Asn | |
| 115 | | | | | | | | 120 | | | | 125 | | | | |
| Ile | Lys | Ser | Glu | Ile | Lys | Lys | Leu | Glu | Asn | Gln | Leu | Ile | Glu | Thr | Thr | |
| 130 | | | | 135 | | | | | | | | 140 | | | | |
| Thr | Arg | Leu | Leu | Thr | Ser | Tyr | Gln | Ile | Phe | Leu | Asn | Gln | Ala | Arg | Asp | |
| 145 | | | | | 150 | | | | 155 | | | | 160 | | | |
| Asn | Ala | Asn | Asn | Gln | Ile | Thr | Lys | Asn | Lys | Thr | Gln | Ser | Leu | Glu | Ala | |
| 165 | | | | | | | | 170 | | | | 175 | | | | |
| Ile | Thr | Gln | Ala | Lys | Asn | Asn | Ala | Asn | Asn | Glu | Ile | Ser | Asn | Thr | Gln | |
| 180 | | | | | | | | 185 | | | | 190 | | | | |
| Thr | Gln | Ala | Ile | Thr | Asn | Ile | Thr | Glu | Ala | Lys | Thr | Asn | Ala | Asn | Asn | |
| 195 | | | | 200 | | | | | | | | 205 | | | | |
| Glu | Ile | Ser | Asn | Asn | Gln | Thr | Gln | Ala | Ile | Thr | Asn | Ile | Asn | Glu | Ala | |
| 210 | | | | 215 | | | | | | | | 220 | | | | |
| Lys | Glu | Ser | Ala | Thr | Thr | Gln | Ile | Asn | Ala | Asn | Lys | Gln | Glu | Ala | Ile | |
| 225 | | | | | 230 | | | | 235 | | | | 240 | | | |
| Asn | Asn | Ile | Thr | Gln | Glu | Lys | Thr | Gln | Ala | Thr | Ser | Glu | Ile | Thr | Glu | |
| 245 | | | | | | | | 250 | | | | 255 | | | | |
| Ala | Lys | Lys | Thr | Asp | His | Tyr | Gln | Asn | Ile | Asp | Phe | Phe | Glu | Phe | Glu | |
| 260 | | | | 265 | | | | | | | | 270 | | | | |

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature

(B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607

| | | | | | | | | | | | | | | | |
|---------|---------|-----|---------|---------|--------|-----|---------|---------|---------|-----|---------|---------|---------|--------|---------|
| Gly 1 | Leu | Ser | Val | Leu 5 | Glu | Arg | Tyr | Ala | Asn 10 | Glu | Glu | Met | Lys | Ala 15 | Leu |
| Trp | Asn | Glu | Gln 20 | Thr | Lys | Phe | Glu | Thr 25 | Tyr | Leu | Glu | Val | Glu 30 | Lys | Ala |
| Val | Val | Arg | Ala 35 | Trp | Asn | Lys | Leu 40 | Gly | Gln | Ile | Gln | Asp | Ser 45 | Asp | Cys |
| Glu | Lys 50 | Ile | Cys | Leu | Lys 55 | Ala | Ala | Phe | Asn | Leu | Glu 60 | Arg | Ile | Lys | Glu |
| Ile 65 | Glu | Lys | Thr | Thr 70 | Lys | His | Asp | Leu | Ile 75 | Ala | Phe | Thr | Thr | Cys | Val 80 |
| Ala | Glu | Ser | Leu 85 | Gly | Glu | Glu | Ser | Arg | Phe 90 | Phe | His | Tyr | Gly 95 | Ile | Thr |
| Ser | Ser | Asp | Cys 100 | Ile | Asp | Thr | Ala | Met 105 | Ala | Leu | Leu | Met | Thr 110 | Lys | Ser |
| Leu | Lys 115 | Leu | Ile | Gln | Lys | Gly | Val 120 | Lys | Asn | Leu | Tyr | Glu 125 | Thr | Leu | Lys |
| Asn | Arg 130 | Ala | Leu | Glu | His | Gln | Asp 135 | Thr | Leu | Met | Val 140 | Gly | Arg | Ser | His |
| Gly 145 | Val | Phe | Gly | Glu 150 | Pro | Ile | Thr | Phe | Gly 155 | Leu | Val | Leu | Ala | Leu | Phe 160 |

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```

Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu Asp Leu Thr Met Glu
      165      170      175
Phe Ile Ser Val Trp Ala Ile Ser Gly Gly Leu Gly Asn Phe Ala His
      180      185      190
Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly Phe Leu Gly Leu Lys
      195      200      205
Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg Asp Arg Tyr Ala Arg
      210      215      220
Leu Ala Cys Asp Leu Ala Leu Leu Ala Ser Ser Cys Glu Lys Ile Ala
      225      230      235      240
Val Asn Ile Arg His Leu Gln Arg Ser Glu Val Tyr Glu Val Glu Glu
      245      250      255
Ala Phe Ser Ala Gly Gln Lys Gly Ser Ser Ala Met Pro His Lys Arg
      260      265      270
Asn Pro Ile Leu Ser Glu Asn Ile Thr Gly Leu Cys Arg Val Ile Arg
      275      280      285
Ser Phe Thr Thr Pro Met Leu Glu Asn Val Ala Leu Trp His Glu Arg
      290      295      300
Asp Met Ser His Ser Ser Val Glu Arg Phe Ala Leu Pro Asp Leu Phe
      305      310      315      320
Ile Thr Ser Asp Phe Met Leu Ser Arg Leu Asn Ser Val Ile Glu Asn
      325      330      335
Leu Val Val Tyr Pro Lys Asn Met Leu Lys Asn Leu Ala Leu Ser Gly
      340      345      350
Gly Leu Val Phe Ser Gln Arg Val Leu Leu Glu Leu Pro Lys Lys Gly
      355      360      365
Leu Ser Arg Glu Glu Ser Tyr Ser Ile Val Gln Glu Asn Ala Met Lys
      370      375      380
Ile Trp Glu Val Leu Gln Gln Gly Ala Phe Lys Asn Ala Asp Glu Asn
      385      390      395      400
Leu Phe Leu Asn Ala Leu Leu Asn Asp Glu Arg Leu Lys Lys Tyr Leu
      405      410      415
Asn Glu Ser Glu Ile Arg Ala Cys Phe Asp Tyr Ser Tyr Tyr Thr Lys
      420      425      430
Asn Val Gly Ala Ile Phe Lys Arg Val Phe Gly
      435      440

```

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608

```

Asn Asp Ser Gly Ser Lys His Phe Ile Leu Pro Phe Leu Thr Leu Leu
1      5      10      15
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
      20      25      30
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
      35      40      45
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys

```

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```

      50              55              60
Asn Ser Thr Arg Ser Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
65              70              75              80
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
      85              90              95
Ile

```

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609

```

Met Glu Lys Phe Phe Asn Gln Phe Phe Glu Asn Ile Gly Glu Asp Lys
1              5              10              15
Asn Arg Glu Gly Leu Lys Glu Thr Pro Lys Arg Val Gln Glu Leu Trp
      20              25              30
Lys Phe Leu Tyr Lys Gly Tyr Lys Glu Asp Pro Arg Val Ala Leu Lys
      35              40              45
Ser Ala Tyr Phe Gln Gly Val Cys Asp Glu Met Ile Val Ala Gln Asn
      50              55              60
Ile Glu Phe Tyr Ser Thr Cys Glu His His Leu Leu Pro Phe Phe Gly
65              70              75              80
Asn Ile Ser Val Gly Tyr Ile Pro Lys Glu Lys Ile Val Gly Ile Ser
      85              90              95
Ala Ile Ala Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln
      100              105              110
Glu Arg Leu Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu
      115              120              125
Pro Arg Gly Val Ile Val Val Cys Glu Ala Lys His Leu Cys Met Ser
      130              135              140
Met Gln Gly Val Gln Lys Gln Asn Ala Ile Ile Lys Thr Ser Val Leu
145              150              155              160
Arg Gly Leu Phe Lys Lys Asp Pro Lys Thr Arg Ala Glu Phe Met Gln
      165              170              175
Leu Leu Lys Ser
      180

```

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610

```

Val Ile Ile Leu Gly Met Ser Asn Pro Asn Leu Ser Phe Tyr Cys Asn
1           5           10           15
Glu Cys Glu Arg Phe Glu Ser Phe Leu Lys Asn His Tyr Leu His Leu
20           25           30
Glu Gly Phe His Pro Tyr Leu Glu Lys Ala Phe Phe Glu Met Val Leu
35           40           45
Asn Gly Gly Lys Arg Phe Arg Pro Lys Leu Phe Leu Ala Val Leu Cys
50           55           60
Ser Leu Val Gly Lys Lys Asp Tyr Ser Asn Gln Gln Thr Glu Tyr Phe
65           70           75           80
Lys Ile Ala Leu Ser Ile Glu Cys Leu His Thr Tyr Ser Leu Ile His
85           90           95
Asp Asp Leu Pro Cys Met Asp Asn Ala Ile Leu Arg Arg Asn His Pro
100          105          110
Thr Leu His Ala Lys Tyr Asp Glu Thr Thr Ala Val Leu Ile Gly Asp
115          120          125
Ala Leu Asn Thr Tyr Ser Phe Glu Leu Leu Ser Asn Ser Leu Leu Glu
130          135          140
Ser Arg Ile Ile Val Glu Leu Val Lys Ile Leu Ser Ala Asn Gly Gly
145          150          155          160
Ile Lys Gly Met Ile Leu Gly Gln Ala Leu Asp Cys Tyr Phe Glu Asn
165          170          175
Thr Pro Leu Asn Leu Glu Gln Leu Thr Phe Leu His Glu His Lys Thr
180          185          190
Ala Lys Leu Ile Ser Ala Ser Leu Ile Met Gly Leu Val Ala Ser Gly
195          200          205
Ile Asn Asp Glu Glu Leu Leu Lys Trp Leu Gln Ala Phe Gly Leu Lys
210          215          220
Met Gly Leu Cys Phe Gln Val Leu Asp Asp Ile Ile Asp Val Thr Gln
225          230          235          240
Asp Glu Lys Glu Ser Gly Lys Thr Thr His Leu Asp Ser Ala Lys Asn
245          250          255
Ser Phe Val Asn Leu Leu Gly Leu Lys Lys Ala Ser Gly Tyr Ala Gln
260          265          270
Thr Leu Lys Thr Glu Ile Leu Asn Asp Leu Asn Ala Leu Glu Pro Thr
275          280          285
Tyr Leu Ser Leu Gln Glu Asn Leu Asn Ala Leu Leu Asn Thr Leu Phe
290          295          300
Lys Gly Lys Thr
305

```

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611

```

Leu Leu Asn Thr Ser Lys Lys Lys Arg Asn Leu Asn Trp Asn Phe Thr
1      5      10      15
Cys Leu Lys Gly Val Met Arg Ala Arg Cys Ser Lys Lys Ser Ser Met
20      25      30
Arg Lys Glu Lys Ile Met Thr Asn Phe Glu Lys Ile Ile Ala Gln Asn
35      40      45
Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe Ala
50      55      60
Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp Leu
65      70      75      80
Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr Ile
85      90      95
Thr Ile Val Met Phe Val Val Ala Phe Val Ile Ile Leu Val Cys Ile
100     105     110
Gln Asn Phe Ser Ser Ile Met Leu Ser Gly Asp Glu Tyr Lys Leu Ile
115     120     125
Asp Pro Ser Lys Val Leu Ser Ser Lys Glu Asn Gln Ile His Arg Leu
130     135     140
Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu His Phe Glu Pro Lys Leu
145     150     155     160
Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala Phe Ala Ser Gly Trp Asp
165     170     175
Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser Ala Leu Ile Glu Arg Leu
180     185     190
Asp Arg Asp Glu Leu Lys Ala Val Ile Ala His Glu Leu Ser His Ile
195     200     205
Arg His Asn Asp Ile Arg Leu Thr Met Cys Val Gly Ile Leu Ser Asn
210     215     220
Ile Met Leu Leu Val Ala Asn Phe Ser Val Tyr Phe Phe Met Gly Asn
225     230     235     240
Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg Met Ile Leu Trp Val Leu
245     250     255
Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu Leu Gln Met Tyr Leu Ser
260     265     270
Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly Ala Ala Phe Leu Met His
275     280     285
Asp Asn Lys Pro Met Ile Arg Ala Leu Gln Lys Ile Ser Asn Asp Tyr
290     295     300
Thr Asn Asn Asp Tyr Lys Lys Glu Ile Asp Lys Asn Ser Thr Arg Ser Ala
305     310     315     320
Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser Thr His Pro Ser Ile Lys
325     330     335
Asn Arg Ile Gln Ser Leu Arg Lys Arg Val Ile
340     345

```

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612

```

Thr Gln Pro His Lys Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
1           5           10           15
Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg Leu Asn Lys Arg
20           25           30
Leu Asn Lys Lys Leu Asn Lys Ser Lys Lys Lys Lys Ile Ser Leu Asn
35           40           45
Lys Thr Val Ser Arg Pro Phe Lys Thr Ile Lys Lys Pro Pro Gln Pro
50           55           60
Pro
65

```

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613

```

Gly Val Asn Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg
1           5           10           15
Phe Val Phe Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn
20           25           30
Asp Ile Val Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln
35           40           45
Tyr Cys Cys Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His
50           55           60
Lys Ile Glu Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu
65           70           75           80
Tyr Cys Ile Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His
85           90           95
Ala Thr Asn Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe
100          105          110
Asn Asp Thr Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly
115          120          125
Val Ile Ser Lys Asp Ser Leu Leu Lys
130          135

```

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614

```

Phe Lys Cys Asn Leu Lys Arg Arg Ser Ala Leu Lys Leu Leu Val Val
1      5      10      15
Asp Asp Ser Ser Thr Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg
      20      25      30
Leu Gly Tyr Glu Asp Val Leu Glu Ala Glu His Gly Val Glu Ala Trp
      35      40      45
Glu Lys Leu Asp Ala Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp
      50      55      60
Asn Met Pro Glu Met Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala
      65      70      75      80
Asp Asn Arg Phe Lys Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly
      85      90      95
Gly Lys Ala Glu Val Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr
      100      105      110
Ile Val Lys Pro Phe Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val
      115      120      125
Val Leu Gly Thr Asn Asp
130

```

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615

```

Arg Val Met Ala Val Arg Ile Met Ala Thr Val Trp Thr Asn Ser Cys
1      5      10      15
Lys Glu Phe Gly Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu Val
      20      25      30
Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys Asn
      35      40      45
Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser Ala
      50      55      60
Phe Val Tyr Ser Leu Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr Phe
      65      70      75      80

```

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```

Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe Leu
      85                      90                      95
Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu Glu
      100                    105                    110
Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln Ile
      115                    120                    125
Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val Pro
      130                    135                    140
Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Ser Ala Ser
      145                    150                    155                    160
Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu Gly
      165                    170                    175
Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro Phe
      180                    185                    190
Ser Tyr Gln Val Ser Ala Thr Phe Gln Asn Ser Arg Leu Ser Ser Leu
      195                    200                    205
Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu Ser
      210                    215                    220
Ser Ala Asn Lys Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe Leu
      225                    230                    235                    240
Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn Phe
      245                    250                    255
Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys Pro
      260                    265                    270
Cys Ala Phe Ala Arg Leu Arg Pro
      275                    280

```

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616

```

Arg Ala Ser His Lys Leu Pro Leu Arg Val Arg Ser Ala Thr Pro Ile
1      5      10      15
Ala Leu Val Ile Gly Val Phe Lys Asn Pro Leu Ile Val Phe Lys Glu
      20      25      30
Ala Leu Phe Leu Glu Thr Leu Ala Lys Val Lys Lys Ile Phe Ile Asp
      35      40      45
Lys Thr Gly Thr Leu Thr Gln Lys Glu Val Leu Leu Lys Glu Lys Ile
      50      55      60
Ile His Glu Glu Phe Asp Glu Arg Leu Leu Lys Ser Leu Leu Lys Thr
      65      70      75      80
Arg Glu His Leu Ala His Asn Ala Ile Leu Lys Thr Leu Asp Gly Asp
      85      90      95
Glu Val Asp Leu Glu Lys Ile Glu Phe Ala His Gly Leu Lys Ala
      100     105     110
Ser Tyr Gln Asn Glu Thr Leu Leu Val Gly Ser Leu Lys Phe Leu Asn
      115     120     125
Ala Met Gly Val Asp Leu Lys Val Lys Glu Ser Ala Asn Ile Met Val

```

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```

      130              135              140
Gly Phe Ala Lys Asn Lys Thr Leu Cys Ala Leu Phe Ile Leu Glu Glu
145              150              155              160
Arg Leu Lys Ala Asn Ala Lys Glu Val Ile Gln Ala Leu Gln Asn Gln
      165              170              175
Gly Leu Glu Leu Glu Ile Leu Ser Gly Asp Asn Glu Ser Ser Val Lys
      180              185              190
Glu Cys Ala Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617

```

Thr Pro Thr Lys Ala Pro Lys Ile Val Gln Glu Gln Val Thr Tyr Pro
1      5      10      15
Leu Val Ser Thr Phe Met Ser Ile Ala Asn Ile Asp Thr Val Arg Gly
      20      25      30
Ile Ser Ser Tyr Glu Ser Gly Leu Ile Tyr Ile Ile Phe Lys Asp Gly
      35      40      45
Val Asn Leu Tyr Trp Ala Arg Asp Arg Val Leu Glu Gln Leu Asn Arg
      50      55      60
Val Ser Asn Leu Pro Lys Asp Ala Lys Val Glu Ile Gly Ser Asp Ser
65      70      75      80
Thr Ser Ile Gly Trp Ala Tyr Gln Tyr Ala Leu Ser Ser Asp Ser Lys
      85      90      95
Asn Leu Ser Asp Leu Lys Val Leu Gln Asp Phe Tyr Tyr Arg Tyr Ala
      100      105      110
Leu Leu Gly Val Asp Gly Val Ser Glu Val Ala Ser Val Gly Gly Phe
      115      120      125
Val Lys Asp Tyr Glu Val Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr
      130      135      140
Asn Leu Ser Leu Glu Gln Val Ala Asn Ala Ile Lys Asn Ser Asn Asn
145      150      155      160
Asp Thr Gly Gly Gly Val Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile
      165      170      175
Arg Ser His Gly Tyr Ile Gln Ser Leu Asn Asp Leu Glu Glu Ile Val
      180      185      190
Val Lys Lys Glu Gly Ala Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser
      195      200      205
Val Arg Leu Ala Pro Lys Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly
      210      215      220
Asp Lys Glu Val Val Gly Gly Ile Val Met Val Arg Tyr His Ala Asp
225      230      235      240
Thr Tyr Lys Val Leu Lys Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln
      245      250      255
Ala Ser Asn Pro Asp Val Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu
      260      265      270

```

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```

Leu Ile Glu Lys Gly Ile Asp Asn Leu Ile His Thr Leu Ile Glu Glu
275 280 285
Ser Val Ile Val Leu Val Ile Ile Ala Ile Phe Leu Leu His Phe Arg
290 295 300
Ser Ala Leu Val Val Ile Ile Thr Leu Pro Leu Ser Val Cys Ile Ser
305 310 315 320
Phe Leu Leu Met Arg Tyr Phe Asn Ile Glu Ala Ser Ile Met Ser Leu
325 330 335
Gly Gly Ile Ala Ile Ala Ile Arg Ala Met Val Asp Ala Ala Ile Val
340 345 350
Met Val Glu Asn Ala His Lys His Leu Gln His Ile Asp Thr Arg Asp
355 360 365
Asn Thr Gln Arg Val Asn Ala Ile Met Gln Gly Val Lys His Val Gly
370 375 380
Gly Ala Ile Phe Phe Ala Leu Met Ile Ile Val Val Ser Phe Leu Pro
385 390 395 400
Ile Phe Ala Leu Thr Gly Gln Glu Glu Lys Leu Phe Ala Pro Leu Ala
405 410 415
Tyr Thr Lys Thr Phe Ala Met Leu Val Gly Ala Leu Leu Ser Ile Thr
420 425 430
Ile Val Pro Val Leu Met Val Trp Leu Ile Lys Gly Arg Ile Leu Glu
435 440 445
Glu Ser Glu Ser Pro Val Asn Ala Phe Phe Met Lys Ile Tyr Gly Val
450 455 460
Ser Leu Arg Val Val Leu Lys Phe Arg Tyr Ala Phe Leu Ile Ala Ser
465 470 475 480
Val Leu Gly Leu Gly Gly Leu Val Val Ala Tyr Lys Lys Leu Asn Trp
485 490 495
Glu Phe Ile Pro Gln Ile Asn Glu Gly Val Ile Met Tyr Met Pro Val
500 505 510
Thr Ile Asn Gly Val Gly Ile Asp Thr Ala Leu Glu Tyr Leu Lys Lys
515 520 525
Ser Asn Ala Ala Ile Lys Gln Leu Asp Phe Val Lys Gln Val Phe Gly
530 535 540
Lys Val Gly Arg Ala Asn Thr Ser Thr Asp Ala Ala Gly Leu Gly Met
545 550 555 560
Ile Glu Thr Tyr Ile Glu Leu Lys Pro Gln Asn Glu Trp Lys Glu Lys
565 570 575
Leu Ser Tyr Lys Glu Val Arg Asp Lys Leu Glu Lys Thr Leu Gln Leu
580 585 590
Lys Gly Leu Thr Asn Ser Trp Thr Tyr Pro Ile Arg Gly Arg Thr Asp
595 600 605
Met Leu Leu Thr Gly Ile Arg Thr Pro Leu Gly Ile Lys Leu Tyr Gly
610 615 620
Asn Asp Thr Asp Lys Leu Gln Glu Leu Ala Ile Leu Met Glu Gln Gln
625 630 635 640
Leu Lys Thr Leu Lys Glu Ser Leu Ser Gly Phe Ala Glu Arg Ser Asn
645 650 655
Asn Gly Tyr Tyr Ile Thr Leu Asp Leu Glu Arg
660 665

```

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618

```

Arg Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr
1          5          10          15
Leu His Ala Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp
      20          25          30
Val Ala Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu
      35          40          45
Ser Thr Tyr Ala Arg Ala Met Gly Gly Glu Leu Gln Leu Ala Lys
      50          55          60
Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser
      65          70          75          80
Asn Ala Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
      85          90          95

```

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619

```

Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Ala Ser Leu Asn
1          5          10          15
Ser Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala
      20          25          30
Phe Leu Asn Gly Asn Val Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr
      35          40          45
Gly Tyr Ser Ser Phe Ser Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala
      50          55          60
Asn Asn Ala Asn Phe Gly Val Tyr Ser Arg Phe Phe Ala Asn His Pro
      65          70          75          80
Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser
      85          90          95
Leu Asn Phe Lys Ser Thr Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn
      100          105          110
Tyr Leu Ala Tyr Ser Ala Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe
      115          120          125
Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser
      130          135          140
Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln
      145          150          155          160
Val Ala Leu Lys Asn Gly Ala Ser Ser Gln His Leu Phe Asn Ala Asn
      165          170          175
Ala Thr Trp Lys Arg Val Ile Ile Met Gly Thr Leu His Thr Phe Ile
      180          185          190

```

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Cys Met Arg Glu Phe Tyr Lys Ser Ser Leu Thr Leu Asp Arg Met Met
 195 200 205
 Trp Arg Leu
 210

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Ile | Leu | Ala | Ser | Glu | Leu | Glu | Phe | Lys | Phe | Leu | Ile | Lys | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ile | Met | Ala | His | His | Glu | Glu | Gln | His | Gly | Gly | His | His | His | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | His | His | Thr | His | His | His | His | Tyr | His | Gly | Gly | Glu | His | His | His |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| His | His | His | Ser | Ser | His | His | Glu | Glu | Gly | Cys | Cys | Ser | Thr | Ser | Asp |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Ser | His | His | Gln | Glu | Glu | Gly | Cys | Cys | His | Gly | His | His | Glu | | |
| 65 | | | | 70 | | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Leu | Ile | Arg | Thr | Pro | Lys | His | Leu | Thr | Lys | Gln | Glu | Ser | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Leu | Gly | Ala | Tyr | Tyr | Thr | Pro | Pro | Tyr | Leu | Val | Asp | Cys | Ala | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Leu | Leu | Lys | Lys | His | Val | Gly | Ile | Glu | Asn | Tyr | Thr | Leu | Leu | Asp |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Thr | Ala | Cys | Gly | Asn | Lys | Glu | Phe | Leu | Lys | Leu | His | His | Pro | Lys | Lys |

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| | | |
|---|-----|-----|
| 50 | 55 | 60 |
| Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn Ala | | |
| 65 | 70 | 75 |
| Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu Pro | | |
| | 85 | 90 |
| Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe Ile | | |
| | 100 | 105 |
| Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn Asp | | |
| | 115 | 120 |
| Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala Ile | | |
| | 130 | 135 |
| Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu Ile | | |
| | 145 | 150 |
| Lys Glu Ala Asn Phe Lys Gln Leu Lys Leu Phe Lys Asp His Tyr Arg | | |
| | 165 | 170 |
| Leu Leu Asp Ala Phe Val Val Ser Ser Lys Ser Phe Thr Lys Ser Asn | | |
| | 180 | 185 |
| Glu Phe Pro Ile Val Ile Ala Leu Tyr Glu Arg Gly Arg Met Asp Tyr | | |
| | 195 | 200 |
| Ala Gly Ile Arg Arg Phe Val Phe Pro Thr Asp Cys Asp Thr Thr Leu | | |
| | 210 | 215 |
| Cys Leu Asn Asp Phe Asp Tyr Ile Ala Asn Tyr Val Asp Lys Tyr Pro | | |
| | 225 | 230 |
| Asn Ala Lys Lys Val Gly Ala Cys Val Gly Tyr Phe Phe Pro Met Arg | | |
| | 245 | 250 |
| Asp Ile Asn Ala Leu Lys Arg Asn Lys Thr Phe Leu Asn Ala Pro Ser | | |
| | 260 | 265 |
| Glu Asn Ala Val Arg Ile Ser Gln Asp Lys Leu Ile Tyr Tyr Gln Tyr | | |
| | 275 | 280 |
| Ile His Tyr Phe Lys Glu Ile Ala Pro Lys Ile Pro Tyr Tyr Phe Gly | | |
| | 290 | 295 |
| Asn Leu Asp Ile Ile Ile Asp His Phe Ala Phe Leu Glu Ile Lys Asp | | |
| | 305 | 310 |
| Ala Phe Leu Lys Asp Lys Arg Ala Arg Leu Glu Tyr Phe Lys Lys Leu | | |
| | 325 | 330 |
| Phe Gln Gly His Pro Cys Glu Phe Asp | | |
| | 340 | 345 |

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622

| |
|---|
| Asn Ile Leu Lys Asn Cys Phe Lys Asp Thr Leu Val Ser Leu Ile Lys |
| 1 5 10 15 |
| Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser Ile Pro Leu Thr Ser |
| 20 25 30 |
| Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His Ala Phe Ser Asp Tyr |
| 35 40 45 |

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```

Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe Ser Leu Lys His Tyr
 50          55          60
Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile Lys Asp Lys Glu Lys
 65          70          75          80
Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr His Phe Leu Gly Ala
          85          90          95
Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser Glu Met Ile Tyr Tyr
 100          105          110
Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn Leu Glu Asn Thr Leu
 115          120          125
Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu Asp Asn Phe Met Ile
 130          135          140
Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly Gly Met Asp Phe Glu
 145          150          155          160
Leu Leu Arg Ile Ser Tyr Pro Leu Leu Ile His Ser Phe Asp Asp Asn
          165          170          175
Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln Tyr Gly Ser Lys Thr
          180          185          190
Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu Glu Leu Lys Thr Ala
 195          200          205
Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys Glu His Ala Leu Leu
 210          215          220
Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu Glu Met Leu Lys Ile
 225          230          235          240
Phe Gly Leu Leu Ser Gln Val His His Asn Asp Val Leu Lys Ile Leu
          245          250          255
Glu Lys Ile Leu Gln Asn
          260

```

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623

```

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
 1          5          10          15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
 20          25          30
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
 35          40          45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
 50          55          60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
 65          70          75          80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
          85          90          95
Thr Leu Arg Asp Ala Asn Asn Thr Leu Ile Gln Ala Leu Ile Pro Ile
          100          105          110
Ser Gln Asp Leu Gln Ile His Ile Tyr Lys Lys Gly Glu Asp Tyr Phe
          115

```

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```

      115      120      125
Leu Asp Phe Ile Pro Ile Val Phe Thr Arg Lys Glu Arg Thr Leu Leu
130      135      140
Leu Ser Leu Gln Thr Ser Pro Tyr Gln Asp Ile Val Lys Ala Thr Asn
145      150      155      160
Asp Pro Leu Leu Ala Asn Gln Leu Met Asn Ala Tyr Lys Lys Ser Val
      165      170      175
Pro Phe Lys Arg Leu Val Lys Asn Asp Lys Ile Ala Ile Val Tyr Thr
      180      185      190
Arg Asp Tyr Arg Val Gly Gln Ala Phe Gly Gln Pro Thr Ile Lys Met
      195      200      205
Ala Met Val Ser Ser Arg Leu His Gln Tyr Tyr Leu Phe Ser His Ser
210      215      220
Asn Gly Arg Tyr Tyr Asp Ser Lys Ala Gln Glu Val Ala Gly Phe Leu
225      230      235      240
Leu Glu Thr Pro Val Lys Tyr Thr Arg Ile Ser Ser Pro Phe Ser Tyr
      245      250      255
Gly Arg Phe His Pro Val Leu Lys Val Lys Arg Pro His Tyr Gly Val
      260      265      270
Asp Tyr Ala Ala Lys His Gly Ser Leu Ile His Ser Ala Ser Asp Gly
      275      280      285
Arg Val Gly Phe Ile Gly Val Lys Ala Gly Tyr Gly Lys Val Val Glu
290      295      300
Ile His Leu Asn Glu Leu Arg Leu Val Tyr Ala His Met Ser Ala Phe
305      310      315      320
Ala Asn Gly Leu Lys Lys Gly Ser Phe Val Lys Lys Gly Gln Ile Ile
      325      330      335
Gly Arg Val Gly Ser Thr Gly Leu Ser Thr Gly Pro His Leu His Phe
      340      345      350
Gly Val Tyr Lys Asn Ser Arg Pro Ile Asn Pro Leu Gly Tyr Ile Arg
      355      360      365
Thr Ala Lys Ser Lys Leu His Gly Lys Gln Arg Glu Val Phe Leu Glu
370      375      380
Lys Ala Gln Tyr Ser Lys Gln Lys Leu Glu Glu Leu Phe Lys Thr His
385      390      395      400
Ser Phe Glu Lys Asn Ser Phe Tyr Leu Leu Glu Gly Phe
      405      410

```

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624

```

Gly Cys Leu Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val Cys
1      5      10      15
Gln Leu Glu Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr
20      25      30
Asn Tyr Tyr Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn
35      40      45

```

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```

Asp Leu Ser Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu
 50      55      60
His Ser Trp Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr
 65      70      75      80
Leu Gly Thr Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe
      85      90      95
Gln Trp Tyr His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe Lys
      100      105      110
Phe Gln Ile Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr
      115      120      125
Lys Gly Thr Leu Tyr Leu Ala Tyr Thr Gln Thr Asn Trp Phe Gln Ile
      130      135      140
Tyr Asn Asp Pro Gln Ser Ala Pro Met Arg Met Ile Asn Phe Met Pro
      145      150      155      160
Glu Leu Ile Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly Lys
      165      170      175
Ile Gly Asn Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser Asn
      180      185      190
Gly Val Gly Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly Asn
      195      200      205
Pro Glu Asn Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr Asn
      210      215      220
Gly Gln Lys Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala Gly
      225      230      235      240
Asn Ala Leu Cys Phe Val Trp Cys Gly Lys Arg Glu Ala
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625

```

Met Asn Arg Ala Trp Ile Lys Lys Lys Met Lys Lys Ile Lys Leu Thr
 1      5      10      15
Lys Arg Met Ile Ala Thr Ala Lys Lys Ala Leu Ser Lys Ser Tyr Gly
      20      25      30
Tyr Cys Leu Val Gly Arg Phe Leu Ile Phe Phe Leu Arg Phe Cys Ile
      35      40      45
Phe Phe Trp His Ala Gly Lys Lys Ser Tyr Cys Pro Ser Leu Ala Val
      50      55      60
Lys Lys Thr Arg Lys Pro Gly Cys Arg Gly Ile Glu Ser Phe Tyr Gln
      65      70      75      80
Pro Ser Lys

```

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626

```

Arg Ile Glu Trp Gly Asn Arg His Cys Gly Ala Leu Ser His Ala Asn
1      5      10      15
Ser Val Ser Met Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu
20      25      30
Gly Ile Leu Asn Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met
35      40      45
Leu Gly Val Val Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro
50      55      60
Ile Gln Asn Ala Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val
65      70      75      80
Met Phe Leu Gly Leu Phe Asn Asp Ile Thr Arg Leu Leu
85      90

```

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627

```

Asn Leu Gly Gly Ala Ala Asn Val Ala Asn Asn Leu Thr Ser Leu Lys
1      5      10      15
Ala Lys Val Phe Leu Cys Gly Val Val Gly Asp Asp Leu Lys Gly Lys
20      25      30
His Phe Ile Ser Thr Leu Asn Ser Ile Arg Ile Asp Thr Ser Gly Val
35      40      45
Leu Ile Asp Lys Thr Arg Cys Thr Thr Leu Lys Thr Arg Ile Ile Ala
50      55      60
Gln Asn Gln Gln Ile Val Arg Val Asp Lys Glu Ile Lys Asp Pro Leu
65      70      75      80
Asn Ala Asp Leu Arg Lys Asn Leu Leu Asp Phe Ile Ala Glu Lys Ile
85      90      95
Gln Glu Ile Asp Gly Val Ile Leu Ser Asp Tyr Asn Lys Gly Val Leu
100      105      110

```

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Asp Phe Glu Leu Thr Gln Thr Ile Ile Thr Leu Ala Asn Lys His His
 115 120 125
 Lys Leu Ile Leu Cys Asp Pro Lys Gly Lys Asp Tyr Ser Lys Tyr Ser
 130 135 140
 His Ala Ser Leu Ile Thr Pro Asn Arg Ala Glu Leu Glu Gln Ala Leu
 145 150 155 160
 His Leu Lys Leu Asp Ser His Ala Asn Leu Ser Lys Ala Leu Gln Ile
 165 170 175
 Leu Gln Glu Thr Tyr His Ile Ala Met Pro Leu Val Thr Leu Ser Glu
 180 185 190
 Gln Gly Ile Ala Phe Leu Glu Lys Gly Glu Leu Val Asn Cys Pro Thr
 195 200 205
 Ile Ala Lys Glu Val Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile
 210 215 220
 Ala Ser Leu Thr Leu Ser Leu Leu Glu Ser Lys Ser Leu Lys Glu Ala
 225 230 235 240
 Cys Glu Phe Ala Asn Ala Ala Ala Val Val Val Gly Lys Met Gly
 245 250 255
 Ser Ala Leu Ala Ser Leu Glu Glu Ile Ala Leu Ile Leu Asn Gln Thr
 260 265 270
 His Pro Lys Ile Leu Pro Leu Glu Lys Leu Leu Glu Thr Leu Glu Arg
 275 280 285
 Asn Gln Gln Lys Ile Val Phe Thr Asn Gly Cys Phe Asp Ile Leu His
 290 295 300
 Lys Gly His Ala Ser Tyr Leu Gln Lys Ala Lys Ala Leu Gly Asp Ile
 305 310 315 320
 Leu Val Val Gly Leu Asn Ser Asp Asn Ser Ile Lys Arg Leu Lys Gly
 325 330 335
 Asp Lys Arg Pro Ile Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala
 340 345 350
 Ser Leu Ser Cys Val Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro
 355 360 365
 Ile Lys Leu Ile Gln Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala
 370 375 380
 Asp Tyr Leu Asn Lys Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr
 385 390 395 400
 Arg Leu Ile Glu Phe Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu
 405 410 415
 Lys Ile Lys Arg Thr His Asn Asp
 420

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628

Gly Ser Leu Met Val Asn Val Phe Phe Lys Gln Gln Lys Phe Val Ile
 1 5 10 15
 Lys Lys Arg Phe Asn Asp Phe Asn Gly Phe Asp Ile Glu Glu Asn Glu

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```

      20      25      30
Val Leu Trp Phe Glu Leu Ile Asn Pro Thr Pro Asn Glu Leu Ala Thr
      35      40      45
Leu Ser Gln Glu Tyr Ala Ile His Tyr Asn Thr Asp His Ser Gln Arg
      50      55      60
Val Ser Ser Val Thr Lys Tyr Trp Glu Asp Ser Ser Ser Val Thr Ile
      65      70      75      80
Asn Ala Phe Phe Thr Asn Gln Asp Glu Asn Glu Thr Phe His Met Glu
      85      90      95
Met Ala Thr Phe Ile Leu Ser Asn Asn Ile Leu Phe Thr Ile Tyr Tyr
      100      105      110
Gly Thr Leu Glu Ile Phe Asp Ser Ile Gln Lys Lys Val Leu Ala Ser
      115      120      125
Pro Lys Lys Phe Glu Asp Gly Phe Asp Ile Leu Thr Lys Ile Phe Glu
      130      135      140
Val Tyr Phe Glu Lys Gly Val Glu Cys Leu Glu Trp Ile Asn Lys Gln
      145      150      155      160
Thr Ser Leu Leu Arg Lys Asn Ile Ile Phe Lys Glu Thr Ser Thr His
      165      170      175
Asp Asp Ile Leu Val Arg Leu Ser Asn Leu Gln Glu Phe Asn Val Ala
      180      185      190
Leu Arg Asp Ser Phe Phe Asp Lys Arg Arg Ile Ile Thr Ala Leu Leu
      195      200      205
Arg Ser Asn Lys Val Asp Ser Asp Thr Lys Asn Asn Leu Asn Ile Ile
      210      215      220
Leu Thr Asp Phe Ser Ser Leu Val Glu Ser Thr Thr Val Asn Leu Asn
      225      230      235      240
Ser Leu Asp Asn Ile Gln Asn Leu Phe Ala Ser Gln Val Asn Val Glu
      245      250      255
Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala Met Met
      260      265      270
Pro Pro Thr Leu Ile Gly Thr Ile Tyr Gly Met Asn Phe Lys Phe Met
      275      280      285
Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile Val Met
      290      295      300
Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys Gly Trp
      305      310      315      320
Leu

```

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629

```

Pro Phe Met Glu Phe Leu Ser Ser Leu Leu Asp Ala Leu Ser Thr Pro
1      5      10      15
His Gly Ile Val Ser Leu Ala Thr Leu Thr Leu Leu Glu Ile Val Leu
      20      25      30

```

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Gly Ile Asp Asn Ile Ile Phe Ile Thr Val Met Val Tyr Lys L
 35 40 45
 Lys His Gln Gln Asn Lys Val Met Ile Leu Gly Leu Gly Leu Ala Met
 50 55 60
 Ile Thr Arg Ile Gly Leu Leu Gly Ser Leu Phe Ile Ser His Leu
 65 70 75 80
 Gln Lys Pro Leu Phe Ala Ile Ala Gly Met Ser Phe Ser Trp Arg Asp
 85 90 95
 Val Val Leu Leu Leu Gly Gly Ala Phe Leu Ala Phe Lys Ala Leu Val
 100 105 110
 Glu Leu Lys Glu Gln Ile Tyr Pro Lys Glu Lys Arg Gln Glu Lys Ala
 115 120 125
 Phe Gly Phe Phe Ile Thr Leu Ile Glu Ile Met Phe Leu Asp Ile Val
 130 135 140
 Phe Ser Leu Asp Ser Val Ile Thr Ala Ile Gly Ile Ala Lys His Leu
 145 150 155 160
 Glu Val Met Ala Leu Ala Ile Ile Leu Ser Val Ile Val Met Met Phe
 165 170 175
 Phe Ser Lys Ile Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys
 180 185 190
 Thr Leu Ala Phe Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu
 195 200 205
 Glu Gly Leu His Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile
 210 215 220
 Gly Phe Ala Leu Leu Ile Glu Cys Leu Asn Ile Phe Ile Glu Lys Lys
 225 230 235 240
 Met Lys Lys Ser

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630

Val Tyr Gly Phe Trp Ala Cys Val Leu Cys Gly Phe Lys Phe Gly Phe
 1 5 10 15
 Val Tyr Phe Ala Gln Thr Arg Ala Phe Gln Phe Arg Gln Asn His Ser
 20 25 30
 Phe His Arg Tyr Gln Asn Glu His Asp Phe Arg Pro Val His Ala His
 35 40 45
 Ser Arg Glu Phe Leu Arg Trp Gly Val Gly Glu Ile Leu Gly Ala Leu
 50 55 60
 Leu Gly Val Gly Pro Arg Asn Leu Gly Val Asp Phe Tyr Leu Arg Leu
 65 70 75 80
 Cys Leu Asp Leu Ala Phe Ala Phe Phe Arg Leu Ser Lys Leu Ala Leu
 85 90 95
 Tyr Phe Ser Glu Gln Gln Arg Ala Arg Val Leu Phe Gly Phe Asn Asp
 100 105 110
 Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys Arg

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```

      115              120              125
Arg Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser Asp Thr
  130              135              140
Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His
  145              150              155

```

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631

```

Arg Tyr Ser Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu
1      5      10      15
Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp
  20      25      30
Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu Ala Glu Ile
  35      40      45
Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Asp Val Ser Ser
  50      55      60
Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser Asp Met Ser
  65      70      75      80
Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn Leu Ser Ser
  85      90      95
Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala Lys Ser Gly
  100      105      110
His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu Val Glu Lys Val
  115      120      125
Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn Ile Ala Thr
  130      135      140
His Val Ser Gly Thr Thr Met Asn Leu Asp Lys Gln Val Asn Leu Phe
  145      150      155      160
Lys Thr

```

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632

```

Ile Cys Leu Lys Leu Asn Gln Gly Gly Val Tyr Gln Lys Arg Val Gly
1      5      10      15
Leu Leu Lys Val Ser Val Ile Thr Ala Cys Phe Asn Ser Glu Lys Thr
20      25      30
Ile Glu Asp Thr Ile Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile
35      40      45
Glu Tyr Ile Ile Ile Asp Gly Ala Ser Ala Ile Ala Leu
50      55      60

```

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633

```

Asn His Ile Val Arg Gly Val Asp Cys Asp Arg Gly Val Ser Ile Leu
1      5      10      15
Gly Val Ser Leu Asn Ser Arg Val Lys Glu Ile Leu Lys Glu Ser Ala
20      25      30
Leu His Ser Met Gln Asp Ser Leu His Phe Lys Val Lys Glu Val Gln
35      40      45
Ser Val Leu Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met
50      55      60
Leu Pro Glu Asp Thr Lys Arg Glu Ile Lys Ile Gln Leu Leu Lys Asn
65      70      75      80
Phe Ile Leu Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys
85      90      95
Asp Arg Glu Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asp Thr Ile
100      105      110
Lys Leu Met Glu Asn Pro Ser Leu Gly Ser Asn Pro Leu Val Gln Lys
115      120      125
Ala Met Lys Asn Lys Glu Ile Ser Lys Ser Leu Pro Tyr Tyr Arg Lys
130      135      140
Met Pro Asn Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu
145      150      155      160
Phe Lys Glu Asn Thr Gln Glu Val Val Gly Val Leu Met Ile Phe Phe
165      170      175
Ser Ile Asp Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu
180      185      190
Phe Leu Ile Gly Val Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser
195      200      205
Leu Gln Asp Lys Ser Ile Thr Glu Ile Tyr Lys Ser Val Pro Lys Ala
210      215      220
Thr Asn Glu Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu

```

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```

225          230          235          240
Glu Tyr Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu
          245          250          255
Thr Phe Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp
          260          265          270
Met Ile Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly
          275          280          285
Ser Val Arg Phe Val Val Val Ala Ala Ser Ala Ile Met Val Leu Ala
          290          295          300
Leu Ile Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg
305          310          315          320
Leu Glu Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn
          325          330          335
Asn Gln Ala His Ser Ser Asp Ile Lys Leu Val Glu Ala Arg Ser Asn
          340          345          350
Asp Glu Leu Gly Arg Met Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln
          355          360          365
Thr Gln Lys Thr Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile
          370          375          380
Lys Val Val Ser Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr
385          390          395          400
Ala Glu Pro Ala Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Met
          405          410          415
Asp His Ala Leu Phe Ala Arg Lys Arg Gly Thr His Met Pro Ser Ile
          420          425          430
Phe Lys Ile Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile
          435          440          445
Gln Asn Ala Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln
          450          455          460
Glu Ile Gln Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu
465          470          475          480
Ala Asn Asp Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys
          485          490          495
Ala Ser Asn Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile
          500          505          510
Glu Asn Ile Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala
          515          520          525
Met Ile Glu Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg
          530          535          540
Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu
545          550          555          560
Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp
          565          570          575
Glu Val Arg Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile
          580          585          590
Glu Ala Asn Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu
          595          600          605
Ser Ile Lys Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile
          610          615          620
Glu Ala Leu Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp
625          630          635          640
Ser Leu Glu Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu
          645          650          655
Glu Asp Val Asn Lys Lys Gln Phe
          660

```

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634

```

Arg Gly Glu Cys Tyr Phe Glu Arg Glu Ile Gly Leu Met Arg Lys Ile
1      5      10      15
Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile Gly Val Val Tyr Ala
20      25      30
Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly Arg Lys Gln Glu Ser
35      40      45
Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys Ser Lys Glu Leu Lys
50      55      60
Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn Lys Glu Glu Lys Lys
65      70      75      80
Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu Val His His Gly Asp
85      90      95
Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro Lys Ile Lys Gly Ser
100      105      110
Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn Asn Ala Pro Lys Pro
115      120      125
Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu Lys Asn Lys Glu Thr
130      135      140
Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly Asn Pro Asn Asn Ala
145      150      155      160
Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly Gly Ile Ser Leu Leu
165      170      175
Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile Gln Glu Glu Gln Glu
180      185      190
Lys Ser Lys Val Ser Lys Ala Gln Ala Arg Asp Arg Leu Ile Ala Glu
195      200      205
Arg Ile Lys Asn Gln Glu Ile Glu Arg Leu Lys Ile His Val Asp Asp
210      215      220
Asp Lys Leu Asn Gln Glu Met Ala Met Met Ala Gln Gln Gln Gly Met
225      230      235      240
Asp Leu Asp His Phe Lys Gln Met Leu Met Ala Glu Gly His Tyr Lys
245      250      255
Leu Tyr Arg Asp Gln Leu Lys Glu His Leu Glu Met Gln Glu Leu Leu
260      265      270
Arg Asn Ile Leu Leu Thr Asn Val Asp Thr Ser Ser Glu Thr Lys Met
275      280      285
Arg Glu Tyr Tyr Asn Lys His Lys Glu Gln Phe Ser Ile Pro Thr Glu
290      295      300
Ile Glu Thr Val Arg Tyr Thr Ser Thr Asn Gln Glu Asp Leu Glu Arg
305      310      315      320
Ala Met Ala Asp Pro Asn Leu Glu Val Pro Gly Val Ser Lys Ala Asn
325      330      335
Glu Lys Ile Glu Met Lys Thr Leu Asn Pro Gln Ile Ala Gln Val Phe
340      345      350
Ile Ser His Glu Gln Gly Ser Phe Thr Pro Val Met Asn Gly Gly Gly
355      360      365
Gly Gln Phe Ile Thr Phe Tyr Ile Lys Glu Lys Arg Gly Lys Asn Glu
370      375      380
Val Ser Phe Ser Gln Ala Lys Gln Phe Ile Ala Gln Lys Leu Val Glu
385      390      395      400
Glu Ser Lys Asp Lys Ile Leu Glu Glu His Phe Glu Lys Leu Arg Val
405      410      415
Lys Ser Arg Ile Val Met Ile Arg Glu

```

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425

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635

```

Ile Val Gln His Phe Asn Phe Leu Tyr Lys Asp Ser Leu Phe Ser Ile
1      5      10      15
Ala Leu Phe Thr Phe Ile Ile Ala Leu Val Ile Leu Leu Glu Gln Ala
20      25      30
Arg Ala Tyr Phe Thr Arg Lys Arg Asn Lys Lys Phe Leu Gln Lys Phe
35      40      45
Ala Gln Asn Gln Asn Ala Tyr Ala Ser Ser Glu Asn Leu Asp Glu Leu
50      55      60
Leu Lys His Ala Lys Ile Ser Ser Leu Met Phe Leu Ala Arg Ala Tyr
65      70      75      80
Ser Lys Ala Asp Val Glu Met Ser Ile Glu Ile Leu Lys Gly Leu Leu
85      90      95
Asn Arg Pro Leu Lys Asp Glu Glu Lys Ile Ala Val Leu Asp Leu Leu
100     105     110
Ala Lys Asn Tyr Phe Ser Val Gly Tyr Leu Gln Lys Thr Lys Asp Thr
115     120     125
Val Lys Glu Ile Leu Arg Phe Ser Pro Arg Asn Val Glu Ala Leu Leu
130     135     140
Lys Leu Leu His Ala Tyr Glu Leu Glu Lys Asp Tyr Ser Lys Ala Leu
145     150     155     160
Glu Thr Leu Glu Cys Leu Glu Glu Leu Glu Val Pro Lys Ile Glu Thr
165     170     175
Ile Lys Asn Tyr Leu Tyr Leu Met His Leu Ile Glu Asn Lys Glu Asp
180     185     190
Ala Ala Lys Ile Leu His Val Ser Lys Ala Ser Leu Asp Leu Lys Lys
195     200     205
Ile Ala Leu Asn His Leu Lys Ser His Asp Glu Asn Leu Phe Trp Gln
210     215     220
Glu Ile Asp Thr Thr Glu Arg Leu Glu Asn Val Ile Asp Leu Leu Trp
225     230     235     240
Asp Met Asn Ile Pro Ala Phe Ile Leu Glu Lys His Ala Leu Leu Gln
245     250     255
Asp Ile Ala Arg Ser Gln Gly Leu Leu Leu Asp His Lys Pro Cys Gln
260     265     270
Ile Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys
275     280     285
Ala Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe
290     295     300
Pro Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met
305     310     315     320
Asp Met Val Leu Lys Ile Ser Lys Lys Thr His Ala Met Gly Val Asp
325     330     335

```

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(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636

```

Ile Arg Gly Ala Lys Thr Gly Gln Asn Asp His Leu Lys Gly Lys Met
1          5          10          15
Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp Asn
20          25          30
Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp Lys
35          40          45
Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala Leu
50          55          60
Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu Val
65          70          75          80
Ile Gly Glu Leu Leu Tyr His Lys Phe Tyr Gln Tyr Asp Glu Gly Lys
85          90          95
Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr Lys
100          105          110
Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser Ser
115          120          125
Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser Ala
130          135          140
Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala Lys
145          150          155          160
Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg Leu
165          170          175
Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu Leu
180          185          190
Thr Gln Ala Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln Glu
195          200          205
Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile Gln
210          215          220
Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala Glu
225          230          235          240
Gln Gln Cys Ala Tyr Gln Ala Leu Gln Lys Leu Lys Glu Val Lys
245          250          255

```

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637

```

Ala His Gln Ser Ser Arg Gly Val Ser Met Ile Leu Ala Cys Asp Val
1          5          10          15
Gly Leu Lys Arg Ile Gly Ile Ala Ala Leu Leu Asn Gly Val Ile Leu
20          25          30
Pro Leu Glu Ala Ile Leu Arg His Asn Arg Asn Gln Ala Ser Arg Asp
35          40          45
Leu Ser Asp Leu Leu Arg Lys Lys Asp Ile Gln Val Leu Val Val Gly
50          55          60
Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala Arg Ile Glu His Phe
65          70          75          80
Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val Phe Ile Asn Glu Asp
85          90          95
Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu His Leu Gly Lys Lys
100         105         110
Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu Asp Ser Leu Ser Ala
115         120         125
Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val Leu Lys Lys Gly
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638

```

Lys Asn Glu Asn Phe Ile Lys Val Leu Ile Leu Asp Leu Lys Val Leu
1          5          10          15
Leu Gln Arg Ile Val Asp Phe Phe Ile Lys Leu Asn Lys Lys Gln Lys
20          25          30
Ile Ala Leu Ile Ala Ala Gly Val Leu Ile Thr Ala Leu Val Phe
35          40          45
Leu Leu Leu Tyr Pro Phe Lys Glu Lys Asp Tyr Ala Gln Gly Gly Tyr
50          55          60
Gly Val Leu Phe Glu Arg Leu Asp Ser Ser Asp Asn Ala Leu Ile Leu
65          70          75          80
Gln His Leu Gln Gln Asn Gln Ile Pro Tyr Lys Val Leu Lys Asp Asp
85          90          95
Thr Ile Leu Val Pro Lys Asp Lys Val Tyr Glu Glu Arg Ile Thr Leu
100         105         110

```

SUBSTITUTE SHEET (RULE 26)

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Ala Ser Gln Gly Ile Pro Lys Thr Ser Lys Val Gly Phe Glu Ile Phe
 115 120 125
 Asp Thr Lys Asp Phe Gly Ala Thr Asp Phe Asp Gln Asn Ile Lys Leu
 130 135 140
 Ile Arg Ala Ile Glu Gly Glu Leu Ser Arg Thr Ile Glu Ser Leu Asn
 145 150 155 160
 Pro Ile Leu Lys Ala Asn Val His Ile Ala Ile Pro Lys Asp Ser Val
 165 170 175
 Phe Val Ala Lys Glu Val Pro Pro Ser Ala Ser Val Met Leu Lys Leu
 180 185 190
 Lys Pro Asp Met Lys Leu Ser Pro Thr Gln Ile Leu Gly Ile Lys Asn
 195 200 205
 Leu Ile Ala Ala Ala Val Pro Lys Leu Thr Ile Glu Asn Val Lys Ile
 210 215 220
 Val Asn Glu Asn Gly Glu Ser Ile Gly Glu Gly Asp Ile Leu Glu Asn
 225 230 235 240
 Ser Lys Glu Leu Ala Leu Glu Gln Leu Arg Tyr Lys Gln Asn Phe Glu
 245 250 255
 Asn Ile Leu Glu Asn Lys Ile Val Asn Ile Leu Ala Pro Ile Val Gly
 260 265 270
 Gly Lys Asn Lys Val Val Ala Arg Val Asn Ala Glu Phe Asp Phe Ser
 275 280 285
 Gln Lys Lys Ser Thr Lys Glu Thr Phe Asp Pro Asn Asn Val Val Arg
 290 295 300
 Ser Glu Gln Asn Leu Glu Glu Lys Lys Glu Gly Ala Pro Lys Lys Gln
 305 310 315 320
 Val Gly Gly Val Pro Gly Val Val Ser Asn Ile Gly Pro Val Gln Gly
 325 330 335
 Leu Lys Asp Asn Lys Glu Pro Glu Lys Tyr Glu Lys Ser Gln Asn Thr
 340 345 350
 Thr Asn Tyr Glu Val Gly Lys Thr Ile Ile Glu Ile Lys Gly Glu Phe
 355 360 365
 Gly Thr Leu Met Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr
 370 375 380
 Lys Ile Ala Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu
 385 390 395 400
 Ser Asp Glu Ser Leu Lys Lys Ile Asn Ala Leu Val Lys Gln Ala Ile
 405 410 415
 Gly Asp Asn Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu
 420 425 430
 Phe Asn Pro Met Ala Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys
 435 440 445
 Ile Met His Lys Thr Gln Lys Ile Leu Gly Ser Phe Thr Pro Leu Ile
 450 455 460
 Lys Tyr Ile Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val
 465 470 475 480
 Ile Val Pro Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp
 485 490 495
 Lys Glu Val Lys Ser Met Phe Glu Glu Met Asp Glu Glu Glu Asp Glu
 500 505 510
 Leu Asn Lys Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly
 515 520 525
 Leu Asn Ala Ser Phe Ser Glu Glu Glu Val Arg Tyr Glu Ile Ile Leu
 530 535 540
 Glu Lys Ile Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr
 545 550 555 560
 Leu Phe Lys Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys
 565 570 575
 Gly

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639

```

Lys Trp Cys Gly Tyr Cys Glu Arg Arg Ser Val Arg Arg Gly Tyr Tyr
1      5      10      15
Arg Ser Arg Lys Arg Leu Thr Lys Asn His His Ala Phe Ala Cys Ser
20      25      30
Leu Asp Phe Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile
35      40      45
Ala Gln Asn Gly Leu Ile Leu Ser Glu His Glu Lys Asp Phe Met Phe
50      55      60
Ile Lys Gly Phe Phe Leu Val Arg Asn Cys Leu Val Ile Ala Leu Thr
65      70      75      80
Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser
85      90      95
Ser Val Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro
100     105     110
Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly
115     120     125
Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu
130     135     140
Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu Phe Leu
145     150     155     160
Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe
165     170     175
Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile
180     185     190
Asn His Leu Val Val Leu Ala
195
  
```

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640

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1187

```

Arg Leu Lys Met Ala Thr Lys Leu Thr Pro Lys Gln Lys Ala Gln Leu
1      5      10      15
Asp Glu Leu Ser Met Ser Glu Lys Ile Ala Ile Leu Leu Ile Gln Val
20     25     30
Gly Glu Asp Thr Thr Gly Glu Ile Leu Arg His Leu Asp Ile Asp Ser
35     40     45
Ile Thr Glu Ile Ser Lys Gln Ile Val Gln Leu Asn Gly Thr Asp Lys
50     55     60
Gln Ile Gly Ala Ala Val Leu Glu Glu Phe Phe Ala Ile Phe Gln Ser
65     70     75     80
Asn Gln Tyr Ile Asn Thr Gly Gly Leu Glu Tyr Ala Arg Glu Leu Leu
85     90     95
Thr Arg Thr Leu Gly Ser Glu Glu Ala Arg Lys Val Met Asp Lys Leu
100    105    110
Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala Tyr Leu Gly Lys Ile
115    120    125
Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn Glu His Pro Gln Thr
130    135    140
Ile Ala Leu Ile Leu Ala His Met Glu Ala Pro Asn Ala Ala Glu Thr
145    150    155    160
Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu Ile Ser Ile Arg Met
165    170    175
Ala Asn Leu Gly Glu Ile Ser Pro Gln Val Val Lys Arg Val Ser Thr
180    185    190
Val Leu Glu Asn Lys Leu Glu Ser Leu Thr Ser Tyr Lys Ile Glu Val
195    200    205
Gly Gly Leu Arg Ala Val Ala Glu Ile Phe Asn Arg Leu Gly Gln Lys
210    215    220
Ser Ala Lys Thr Thr Leu Ala Arg Ile Glu Ser Val Asp Asn Lys Leu
225    230    235    240
Ala Gly Ala Ile Lys Glu Met Met Phe Thr Phe Glu Asp Ile Ala Lys
245    250    255
Leu Asp Asn Phe Ala Ile Met Arg Asp Phe Lys Ser Gly Gly Leu Lys
260    265    270
Lys Thr Gly Leu
275

```

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641

```

Arg Ser Leu Gly Lys Gly Arg Pro Met Asn Lys Lys Asn Ser Val Ile
1      5      10      15
Ser Gly Leu Met Asn Phe Phe Ser Glu Lys Asn Glu Arg Trp Leu Leu
20     25     30
Ala His Arg His Thr Arg Gly Phe Val Ile Val Ala Trp Leu Phe Arg
35     40     45
Phe Lys Ser Ile Ala Phe Ser Ile Leu Ile Thr Leu Leu Val Ile Leu

```

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1188

```

50          55          60
Val Asp Ile Trp Val Tyr Ser Asp Val Arg Gln Phe Leu Leu Asp Thr
65          70          75          80
Ser Ser Ser Phe Ile Trp Leu Leu Ile Ala Leu Leu Ile Lys Trp Gly
85          90          95
Val Ile Val Ile Ser Ala Arg Lys Cys Tyr Gln Phe Ser Gln Lys Met
100         105         110
Phe Ala Leu Ile Gln Arg Lys Arg Gln Ile Arg Glu Asn Leu Lys Asn
115         120         125
Arg Ser Asn Arg Lys Asp Ala Lys Asn Phe Glu Lys Leu Ser Asn Ile
130         135         140
Ala Glu Glu Ile Ile Ser Lys Lys Gln Glu Glu Ser His His Lys Glu
145         150         155         160
Asp Ser Asn Asp Glu Asn His Lys Asp Lys Leu Ser Asn Ile Thr Glu
165         170         175
Glu Met Ile Leu Lys Lys Gln Glu Glu Leu Lys Ala Arg Lys Asp Lys
180         185         190
Gly Asp

```

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642

```

Leu Met Asp Arg Ala Lys Phe Ile Phe Val Thr Gly Gly Val Leu Ser
1          5          10          15
Ser Leu Gly Lys Gly Ile Ser Ser Ser Ile Ala Thr Leu Leu Gln
20         25         30
His Cys Asn Tyr Gln Val Ser Ile Leu Lys Ile Asp Pro Tyr Ile Asn
35         40         45
Ile Asp Pro Gly Thr Met Ser Pro Leu Glu His Gly Glu Val Phe Val
50         55         60
Thr Ser Asp Gly Ala Glu Thr Asp Leu Asp Ile Gly His Tyr Glu Arg
65         70         75         80
Phe Leu Asn Arg Asn Leu Thr Arg Leu Asn Asn Phe Thr Thr Gly Gln
85         90         95
Ile Phe Ser Ser Val Ile Glu Asn Glu Arg Lys Gly Glu Tyr Leu Gly
100        105        110
Lys Thr Ile Gln Ile Val Pro His Val Thr Asp Glu Ile Lys Arg Arg
115        120        125
Ile Lys Ser Ala Ala Lys Gly Leu Asp Phe Leu Ile Val Glu Val Gly
130        135        140
Gly Thr Val Gly Asp Met Glu Gly Met Phe Tyr Val Glu Pro Ile Arg
145        150        155        160
Gln Leu Lys Leu Glu Leu Arg Asn Lys Ala Leu Ile Asn Met His Val
165        170        175
Thr Leu Met Pro Tyr Ile Arg Ala Thr Ser Glu Leu Arg Ser Arg Pro
180        185        190

```

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1189

Thr Gln His Ser Val Gln Glu Leu Arg Arg Leu Gly Val Thr Pro Gln
 195 200 205
 Ile Ile Leu Ala Arg Ser Pro Lys Pro Leu Asp Lys Glu Leu Lys Lys
 210 215 220
 Lys Ile Ala Leu Ser Cys Asp Val Glu Gln Asp Ser Val Ile Val Ala
 225 230 235 240
 Thr Asp Thr Lys Ser Ile Tyr Ala Cys Pro Ile Leu Phe Leu Gln Glu
 245 250 255
 Gly Ile Leu Thr Pro Ile Ala Arg Arg Phe Asn Leu Asn Lys Leu His
 260 265 270
 Pro Lys Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro
 275 280 285
 Lys His Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys
 290 295 300
 Glu Ser Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His
 305 310 315 320
 Leu Asp Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn
 325 330 335
 Glu Lys Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly
 340 345 350
 Phe Gly Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala
 355 360 365
 Arg Leu Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu
 370 375 380
 Ala Ile Val Glu Phe Cys Arg Asn Val Leu Gly Leu Lys Gly Ala Asn
 385 390 395 400
 Ser Thr Glu Phe Asn Gln Arg Cys Glu Tyr Pro Val Val Tyr Leu Ile
 405 410 415
 Glu Asp Phe Met Asp Gln Asn His Gln Lys Gln Val Arg Thr Tyr Asn
 420 425 430
 Ser Pro Leu Gly Gly Thr Met Arg Leu Gly Glu Tyr Glu Cys Glu Ile
 435 440 445
 Met Pro Asn Ser Leu Leu Glu Lys Ala Tyr Lys Lys Pro Asn Ile Lys
 450 455 460
 Glu Arg His Arg His Arg Tyr Glu Ile Asn Pro Lys Tyr Arg Gln Glu
 465 470 475 480
 Trp Glu Asn Lys Gly Leu Lys Val Val Gly Phe Gly Ala Asn His Leu
 485 490 495
 Ile Glu Ala Ile Glu Leu Glu Asp His Pro Phe Phe Val Gly Val Gln
 500 505 510
 Phe His Pro Glu Phe Thr Ser Arg Leu Gln Ser Pro Asn Pro Ile Ile
 515 520 525
 Leu Asp Phe Ile Lys Ser Ala Leu His Lys Ser
 530 535

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643

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1190

```

Ile Trp Arg Gly Cys Gly Ser His Asp Arg Val His Asp Glu Phe Val
1      5      10      15
Phe Ala Arg Tyr Thr Lys Ala Asn Tyr Glu Asn Thr Tyr Tyr Asp Thr
20      25      30
Glu Phe Ser His Leu Lys Glu Ala Ser Ala Tyr Phe Pro Asp Ile Asp
35      40      45
Glu Ala Ser Leu Phe Thr Asp Leu Gln Asp Tyr Phe Asn Ser Trp Lys
50      55      60
Glu Leu Ser Lys Asn Ala Lys Asp Ser Ala Gln Lys Gln Ala Leu Ala
65      70      75      80
Gln Lys Thr Glu Ala Leu Thr His Asn Ile Lys Asp Thr Arg Glu Arg
85      90      95
Leu Thr Thr Leu Gln His Lys Ala Ser Glu Glu Leu Lys Ser Val Ile
100      105      110
Lys Glu Val Asn Ser Leu Gly Ser Gln Ile Ala Glu Ile Asn Lys Arg
115      120      125
Ile Lys Glu Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu
130      135      140
Arg Asp Lys Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Leu Gly
145      150      155      160
Gly Asn Val Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys
165      170      175
Asp Ser Ala Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly
180      185      190
Phe Asn Ile Ile Asp Gly Ser Ile Phe His Pro Leu Val Val Lys Glu
195      200      205
Ser Glu Asn Lys Gly Gly Leu Asn Gln Val Tyr Phe Gln Ser Asp Asp
210      215      220
Phe Lys Leu Thr Asn Ile Thr Asp Lys Leu Asn Gln Gly Lys Val Gly
225      230      235      240
Ala Leu Leu Asn Val Tyr Asn Asp Gly Ser Asn Gly Thr Leu Lys Gly
245      250      255
Lys Leu Gln Asp Tyr Ile Asp Leu Leu Asp Ser Phe Ala Arg Gly Leu
260      265      270
Ile Glu Ser Thr Asn Ala Ile Tyr Ala Gln Ser Ala Ser His His Ile
275      280      285
Glu Gly Glu Pro Val Glu Phe Asn Ser Asp Glu Ala Phe Lys Asp Thr
290      295      300
Asn Tyr Asn Ile Lys Asn Gly Ser Phe Asp Leu Ile Ala Tyr Asn Thr
305      310      315      320
Asp Gly Lys Glu Ile Ala Arg Lys Thr Ile Ala Ile Thr Pro Ile Thr
325      330      335
Thr Met Asn Asp Ile Ile Gln Val Ile Asn Ala Asn Thr Asp Asp Asn
340      345      350
Gln Asp Asn Asn Thr Glu Asn Asp Phe Asp Glu Leu Phe His Ser Glu
355      360      365
Leu

```

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644

```

Lys Thr Lys Leu Val Phe Met Ile Lys Ala Arg Phe Lys Lys Arg Leu
1      5      10      15
Leu Gly Ser Arg Gly Ala Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys
      20      25      30
Glu Ala Glu Val Val Ala Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser
      35      40      45
Thr Ile Leu Arg Ile Leu Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr
      50      55      60
Ile Glu Ala Asn His Ser Val Trp Leu Asp Thr Gln Lys Lys Ile Phe
65      70      75      80
Leu Lys Pro Gln Gln Arg Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala
      85      90      95
Leu Phe Pro His Leu Asn Val Tyr Gln Asn Ile Ala Phe Ala His Pro
      100     105     110
Lys Asp Lys Asn Lys Ile His Glu Val Leu Arg Leu Met Arg Leu Glu
      115     120     125
Asn Leu Ser Gln Gln Lys Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln
      130     135     140
Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu
145     150     155     160
Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn Glu Val
      165     170     175
Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser Val Leu
      180     185     190
Leu Val Ser His Asp Pro Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe
      195     200     205
Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn Arg Leu
      210     215     220
Phe Ser Asn Arg Leu Leu Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr
225     230     235     240
Cys His Tyr Glu Val Ile Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys
      245     250     255
Leu Asn Pro Thr Phe Lys Leu Asp Phe Ile Gln Asn Lys Lys Phe
      260     265     270

```

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645

```

Gly Leu Ser Ala Thr Ile Leu Gly Met Trp Ile Met Ser Ser Leu Ser
1      5      10      15
Ser Ser Phe Phe His Ser Leu Phe Phe Ile Lys Ser Asn Pro Gly Gln

```

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```

      20      25      30
Leu Leu Lys Gly Trp Gly Ser Lys Ile Phe Phe Ile Asn Arg Lys Phe
      35      40      45
Val Leu Ala Gln Tyr Asn Pro Ser Val Ser Ile Phe Ile Leu Leu Asn
      50      55      60
Arg Val Phe Gly Val Gly Val
      65      70

```

(2) INFORMATION FOR SEQ ID NO:1646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646

```

Ile Gln Arg Ser His Gln Leu Phe Asn Leu Gln Glu Lys Lys Gly Ile
1      5      10      15
Leu Gly Phe Leu His Gln Lys Asn Ile Leu Asn Ile Ala Gln Asn Asp
      20      25      30
Ile His Gln Leu Leu Ile Leu Met Val Val Phe Ser Met Leu Ala Thr
      35      40      45
Pro Phe Ile Leu Lys Tyr Leu Glu Ser Ile Ala Gln Phe Ile Leu His
      50      55      60
Gln Lys Ser Gln Glu Asn Glu Pro Ala Lys Lys
      65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647

```

Gly Leu Met Arg Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala
1      5      10      15
Phe Leu Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala
      20      25      30

```

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```

Phe Asn Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu
  35          40          45
Ile Leu Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu
  50          55          60
Lys Arg Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys
  65          70          75          80
Met Ile Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln
          85          90          95
Ala Lys Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln
          100          105          110
Met Lys Lys Tyr Ser
          115

```

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648

```

Arg Lys Lys Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu
  1          5          10          15
Phe Tyr Phe Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn
          20          25          30
Pro Lys Thr Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu
          35          40          45
Leu Val Gln Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly
          50          55          60
Ala Tyr Met Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu
          65          70          75          80
Asp Asn Ala Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu
          85          90          95
Asn Ser Glu Gln Gln Asn Leu Gly Gln Arg Ala Ser Gln
          100          105

```

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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1194

(A) NAME/KEY: misc_feature
(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649

```

Met Pro Asn Asn Ala Leu Leu Gln Ile Lys Gln Asp Thr Leu Ser Leu
1      5      10      15
Ile Asp Asp Leu Lys Val Ile Cys Lys Asp Ala Gly Leu Ala Gly Asp
20      25      30
Gly Asn Gly Tyr Lys Ile Ile Thr Gln Cys Phe Leu Tyr Lys Phe Leu
35      40      45
Cys Asp Lys Phe Glu Phe Phe Phe Glu Gln Lys Phe Pro Asn Lys Thr
50      55      60
Ile Arg Asp Tyr Lys Asp Phe Asn Glu Glu Glu Lys Glu Tyr Phe Phe
65      70      75      80
Leu Thr Leu Ser Asp Lys Lys Leu Pro Lys Leu Ala Tyr Asp Glu Leu
85      90      95
Leu Asn Tyr Leu Phe Glu Lys His Phe Tyr Asp Asn Asp Leu His Leu
100     105     110
Lys Leu Asp Ala Ile Phe Asn Arg Ile Ser Ser Asn Asn Ala Glu Leu
115     120     125
Phe Asn Thr Lys Ser Thr Asp Glu Thr Thr Ile Ala Leu Phe Glu Ser
130     135     140
Val Ser Gln Tyr Ile Asn Glu Gly Ser Lys Arg Ala Asn Phe Thr Arg
145     150     155     160
Ser Leu Leu Asp Lys Leu Lys Asn Phe Asn Phe Lys Gln Ala Phe Leu
165     170     175
Asn Leu Gln Asn Gln Gln Gly Tyr Asp Phe Phe Ala Pro Ile Phe Glu
180     185     190
Tyr Leu Leu Lys Asp Tyr Asn Asn Asn Ser Gly Gly Thr Tyr Ala Glu
195     200     205
Tyr Tyr Thr Pro Leu Ser Ile Ala Ser Ile Ile Ala Lys Leu Leu Val
210     215     220
Asn Lys Pro Thr Gln Ser Val Lys Ile Tyr Asp Pro Ser Ala Gly Thr
225     230     235     240
Gly Thr Leu Leu Met Ala Leu Ala His Gln Ile Gly Thr Asp Ser Cys
245     250     255
Thr Leu Tyr Ala Gln Asp Ile Ser Gln Lys Ser Leu Arg Met Leu Lys
260     265     270
Leu Asn Leu Ile Leu Asn Asp Leu Thr His Ser Leu Arg His Ala Ile
275     280     285
Glu Gly Asn Thr Leu Thr Asn Pro Tyr His Ser Lys Asp His Lys Gly
290     295     300
Lys Met Asp Phe Ile Val Ser Asn Pro Pro Phe Lys Leu Asp Phe Ser
305     310     315     320
Asn Glu His Ala Glu Ile Ser Gln Asn Lys Asn Asp Phe Phe Leu Gly
325     330     335
Val Pro Asn Ile Pro Lys Asn Asp Lys Ser Lys Met Pro Ile Tyr Thr
340     345     350
Leu Phe Phe Gln His Cys Leu Asn Met Leu Ser Pro Lys Gly Lys Gly
355     360     365
Ala Ile Ile Val Pro Thr Gly Phe Ile Ser Ala Lys Ser Gly Val Asn
370     375     380
Asn Lys Asn Val Arg His Leu Val Asp Glu Arg Leu Val Tyr Gly Val
385     390     395     400
Ile Cys Met Pro Ser Gln Val Phe Ala Asn Thr Gly Thr Asn Val Ser
405     410     415
Ile Ile Phe Phe Gln Lys Thr Pro Ser Ala Lys Glu Val Ile Leu Ile
420     425     430
Asp Ala Ser Lys Leu Gly Glu Glu Tyr Thr Glu Asn Lys Asn Lys Lys
435     440     445
Thr Arg Leu Arg Pro Ser Asp Met Asp Leu Ile Leu Glu Thr Phe Gln
450     455     460
Asn Lys Ala Pro Lys Ser Asp Phe Cys Ala Leu Val Ser Phe Asp Glu
465     470     475     480

```

SUBSTITUTE SHEET (RULE 26)

1195

```

Ile Thr Glu Lys Asn Tyr Ser Leu Asn Pro Gly Gln Tyr Phe Thr Ile
      485      490      495
Glu Asp Thr Ser Glu Thr Ile Ser Gln Ala Glu Phe Glu Asn Leu Met
      500      505      510
Gln Gln Tyr Ser Ser Glu Leu Ala Ser Leu Phe Asp Glu Ser Gln Asn
      515      520      525
Leu Gln Gln Glu Ile Leu Glu Thr Leu Lys Gly Val Arg Phe Glu
      530      535      540

```

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650

```

Lys Gly Asp Phe Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe
1      5      10      15
Glu Asn Lys Glu Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu
      20      25      30
Val Gln Glu Phe Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp
      35      40      45
Ala Ala Lys Phe Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu
      50      55      60
Lys Ile Ser Arg Ala Met Ala Tyr Ala Gln Leu Leu Phe Ala Lys Asn
      65      70      75      80
Thr Lys Glu Ala Lys Phe Tyr Ser Gln Cys Glu Met Ala Cys Ala Asn
      85      90      95
Ile Gln Gln His Leu Leu Phe Phe Glu Ile Glu Phe Lys Asn Leu Asp
      100     105     110
Ala Lys Lys Gln Leu Ala Phe Ile Lys Lys Cys Lys Asp His Ala Phe
      115     120     125
Tyr Leu Asn Asn Leu Ile Glu Lys Lys Lys His Thr Leu Asn Leu Asp
      130     135     140
Glu Glu Lys Ile Ala Leu Ala Leu Ser Pro Val Gly Val Gly Ala Phe
      145     150     155     160
Ser Phe Val Met Asp Glu His Leu Phe Ser Leu Asn Ile Ser Leu His
      165     170     175
Arg Ile Asn Phe Lys Arg Arg Ile Asn Phe Ser Pro Leu Ala Gln Pro
      180     185     190

```

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651

```

Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys Glu Asn Phe Glu
1      5      10      15
Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly Glu Tyr Thr Lys
20      25      30
Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala Tyr Ala Asp Gly
35      40      45
Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp Val Gly Ala Phe
50      55      60
Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr Asp Asn Phe Glu
65      70      75      80
His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu Glu Ala Lys Asn
85      90      95
Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp Leu Glu Lys Lys
100      105      110
Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met Asn Asp Asn Lys
115      120      125
Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys Ile Ala Leu Ala
130      135      140
Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652

```

Met Pro Phe Leu Lys Ala Leu Ala Ser Phe Asp Ala Pro Phe Leu Glu
1      5      10      15
Lys Glu Ile Ser Lys Arg Phe Arg Asp Asn Leu Val Phe Phe Lys Ser
20      25      30
Tyr His Pro Asn Leu Phe Asn Ala Leu Asn Thr Pro Phe Lys Asn Tyr
35      40      45
Gln Leu Leu Phe Glu Thr Asn His Leu Asn Leu Leu His Thr Pro Thr
50      55      60
Asn Ala Leu Ser Tyr Pro Lys His Gln Met Ile Glu Thr Ala Phe Asn
65      70      75      80
Met Ala Lys Asn Pro Leu Asn Asn Pro Arg Trp Ser Leu Asp Asn Asn
85      90      95

```

1197

His Leu Ser Leu His Tyr Leu Lys Ser Gln Asn Asn His Lys Leu Pro
 100 105 110
 Leu Thr Leu Lys Ala Thr His Ala Ile Ser Asn Phe Leu Asp Asn His
 115 120 125
 Gln Thr Pro Cys Ser Leu Lys Lys Phe Leu Pro Pro Thr Met Ile Tyr
 130 135 140
 Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala Gln Asn Tyr
 145 150 155 160
 Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp Leu Phe Lys
 165 170 175
 Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys Lys Gly Ala
 180 185 190
 Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu Lys Met Asp
 195 200 205
 Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu Glu Ile Met
 210 215 220
 Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn Ile Gln Ser
 225 230 235 240
 Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu Asp Glu Leu
 245 250 255
 Leu Gly Val Lys Asn Thr Leu Lys Asn Leu Pro Leu Cys Gln Thr Leu
 260 265 270
 Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val Val Gly Asn
 275 280 285
 Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu Asn Glu Glu
 290 295 300
 Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro Leu Lys Ala
 305 310 315 320
 His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg Ile Asp Tyr
 325 330 335
 Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr Pro Leu Met
 340 345 350
 Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala Lys Glu Ala
 355 360 365
 Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Tyr Lys Pro Phe Glu
 370 375 380
 Tyr Arg Ile Arg Ser Ala Phe Cys Gly Gln Cys Arg Gly Gly Phe Ser
 385 390 395 400
 Gly Phe Asp Glu Arg
 405

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653

Lys Gly Leu Gly Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu
 1 5 10 15
 Gly Lys Ile Val Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn

SUBSTITUTE SHEET (RULE 26)

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Gly | Asn | Lys | Ile | Ala | Trp | Ile | Thr | Pro | Lys | Asp | Leu | Ser | Thr | Leu | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Gln | Gly | Arg | Tyr | Ile | Lys | Lys | Gly | Ser | Arg | Ser | Ile | Ser | Arg | Leu | Gly | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | |
| Phe | Lys | Ser | Cys | Ser | Cys | Val | Leu | Leu | Pro | Lys | His | Ala | Ile | Leu | Phe | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Ser | Ser | Arg | Ala | Pro | Ile | Gly | Tyr | Val | Ala | Ile | Ala | Glu | Lys | Arg | Leu | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Cys | Thr | Asn | Gln | Gly | Phe | Lys | Ser | Ile | Ile | Pro | Asn | Lys | Lys | Ile | Tyr | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Phe | Glu | Phe | Leu | Tyr | Tyr | Leu | Leu | Lys | Tyr | Tyr | Lys | Asp | Asn | Ile | Ser | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Asn | Ile | Gly | Gly | Gly | Thr | Thr | Phe | Lys | Glu | Val | Ser | Gly | Ala | Thr | Leu | | |
| | | 130 | | | | 135 | | | | | | 140 | | | | | |
| Gly | Leu | Phe | Gln | Val | Lys | Ile | Pro | Pro | Thr | Tyr | Tyr | Glu | Gln | Gln | Lys | | |
| 145 | | | | | 150 | | | | | | 155 | | | | 160 | | |
| Ile | Ala | His | Thr | Leu | Ser | Ile | Leu | Asp | Gln | Lys | Ile | Glu | Asn | Asn | His | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| Lys | Ile | Asn | Glu | Leu | Leu | His | Lys | Ile | Leu | Glu | Leu | Leu | Tyr | Glu | Gln | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| Tyr | Phe | Val | Arg | Phe | Asp | Phe | Leu | Asp | Glu | Asn | Asn | Lys | Pro | Tyr | Gln | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Thr | Ser | Gly | Gly | Lys | Met | Lys | Phe | Ser | Lys | Glu | Leu | Asn | Arg | Leu | Ile | | |
| | | 210 | | | | 215 | | | | | | 220 | | | | | |
| Pro | Asn | Asp | Phe | Lys | Val | Lys | Thr | Leu | Gly | Glu | Leu | Ile | Thr | Trp | Ile | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Ser | Gly | Ser | Gln | Pro | Pro | Lys | Ser | Cys | His | Ile | Tyr | Glu | Tyr | Lys | Glu | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| Gly | Tyr | Ile | Arg | Phe | Ile | Gln | Asn | Arg | Asp | Tyr | Ser | Ser | Asn | Asn | Tyr | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Val | Thr | Tyr | Ile | Pro | Ile | Ser | Lys | Asn | Asn | Lys | Ile | Cys | Tyr | Gln | Tyr | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Asp | Ile | Met | Met | Asp | Lys | Tyr | Gly | Glu | Ala | Gly | Ser | Val | Arg | Phe | Gly | | |
| | | 290 | | | | 295 | | | | | 300 | | | | | | |
| Leu | Gln | Gly | Ala | Tyr | Asn | Val | Ala | Leu | Ser | Lys | Ile | Ser | Val | Leu | Asn | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Gln | Ser | Met | Gln | Glu | Tyr | Ile | Arg | Ser | Tyr | Leu | Asn | Ser | Lys | Pro | Ile | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| Lys | Lys | Tyr | Leu | Ser | Asn | Ala | Cys | Met | Ala | Ser | Thr | Arg | Ala | Ser | Leu | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Asn | G | | | | | | | | | | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

1199

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654

```

Gly Val Thr Leu Ile Gln Gln Glu Gly Phe Ile Met Ile Lys Arg Ile
1           5           10           15
Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala Leu Ala Gly Glu Val
          20           25           30
Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln Gly Arg Tyr Gly Pro
          35           40           45
Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly Asn Asp Leu Tyr Gly
          50           55           60
Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala Asn Lys Trp Phe Gly
65           70           75           80
Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn Thr Ser Gly Thr Glu
          85           90           95
His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly Gly Gly Asp Leu Ile
          100          105          110
Val Asn Leu Ile Pro Ser Asp Lys Phe Ala Leu Gly Leu Ile Gly Gly
          115          120          125
Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro Tyr Asp Val Asn Gln
          130          135          140
Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly Arg Met Arg Val Gly
145          150          155          160
Asp Arg Ser Ala Phe Glu Ala Gly Val Lys Phe Pro Met Val Asn Gln
          165          170          175
Gly Ser Lys Asp Val Gly Leu Ile Arg Tyr Tyr Ser Trp Tyr Val Asp
          180          185          190
Tyr Val Phe Thr Phe
          195

```

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655

```

Phe Arg Phe Tyr Phe Phe Lys Ala Asn Arg Ser Tyr Trp Gly Lys Val
1           5           10           15
Phe Met Val Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu
          20           25           30
Ala Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile
          35           40           45
Ile Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile
          50           55           60
Asn Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe
65           70           75           80
Leu Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser

```

SUBSTITUTE SHEET (RULE 26)

1200

```

      85              90              95
Ile Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys
      100              105              110
Ala Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro
      115              120              125
Ile Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
      130              135              140
Ile Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met
      145              150              155              160
Gly Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile
      165              170              175
Pro Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val
      180              185              190
Asn Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile
      195              200              205
Leu Leu Leu Leu Pro Glu Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln
      210              215              220
Ala Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Val Leu Val
      225              230              235              240
Ile Val Cys Ser Ala Ala Gly Leu Ser His Phe Phe Gly Phe Ser Met
      245              250              255
Ser Leu Gly Ala Phe Ile Val Gly Met Ala Ile Ser Lys Ser Arg Tyr
      260              265              270
Lys Ile Asn Val Gln Glu Glu Phe Ala Gln Leu Lys Asn Leu Phe Leu
      275              280              285
Ala Leu Phe Phe Ile Thr Ile Gly Met Gln Ile Asn Val Ser Phe Phe
      290              295              300
Met Glu Lys Phe Phe Val Val Ile Phe Leu Leu Ile Leu Val Met Ser
      305              310              315              320
Phe Lys Thr Phe Ile Ile Tyr Ala Leu Leu Arg Phe Phe Arg Asp Ala
      325              330              335
Lys Thr Ala Ile Lys Thr Ala Leu Ser Leu Ala Gln Ile Gly Glu Phe
      340              345              350
Ser Phe Val Ile Phe Leu Asn Ser Ala Leu Ala Pro Ala Leu
      355              360              365

```

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656

```

Cys Leu Cys Val Gly Gly Ala Leu Ala His Ile Ser Pro Leu Ser Ile
1      5      10      15
Glu Tyr Ala Ala Pro Phe Val Gly Asn Ala Gly Val Ala Leu Ala Gly
      20      25      30
Leu Met Ser Asp Glu Ile Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile
      35      40      45
Lys Gly Phe Lys Lys His Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys
50      55      60

```

SUBSTITUTE SHEET (RULE 26)

1201

Glu Ile Asp Thr Ser Ser Leu Ile Ser Val Glu Gly Asn Val Glu Gly
 65 70 75 80
 Tyr Glu Thr Phe Ser Asp Ser Leu Phe Leu Ser Lys Glu Arg Ile
 85 90 95
 Glu Glu Ala Leu His Tyr Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser
 100 105 110
 Tyr Gly Ala Lys Ile Lys His Ala Val Ser Leu Asn His Ser Gln Val
 115 120 125
 Lys Leu Lys Gln Ile Asn Lys Gln Asp Ala Ile Val Arg Ile Lys Ser
 130 135 140
 Met Phe Ser Pro Arg Ser Asn His Ala Lys Asp Leu Lys Asn Leu Gln
 145 150 155 160
 Lys Asn Leu Ile Arg Phe Lys Glu Asp Phe Phe Thr His Leu Asn Thr
 165 170 175
 Pro Cys Lys Thr Lys Gln Glu Ala Phe Glu Trp Val Asp Ser Leu Ser
 180 185 190
 Gly Phe Cys Gln Thr Ala Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu
 195 200 205
 Phe Glu Gly Ser Val Ala His Ile Leu Gln Ser Val Leu Ile Val Ser
 210 215 220
 Leu His Leu Lys Glu Asn Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys
 225 230 235 240
 Thr Pro

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657

Ile Leu Leu Val Glu Leu Lys Leu His Pro Lys Ile Gly Tyr Phe Ser
 1 5 10 15
 Lys Arg Phe Asn Phe Leu Ser Lys Met Arg Val Leu Glu Trp Lys Tyr
 20 25 30
 Trp Leu Asn Thr Asp Lys Trp Asp Thr Pro Thr Asn Lys Pro Pro Gln
 35 40 45
 Thr Phe Lys Ile Gln Ile Phe Lys Ile Gln Ile Gly Ile Ile Asn Asn
 50 55 60
 Phe Asn His Leu Ile Lys Gly Ser Ser Met Lys Asn Ala Phe Lys Ala
 65 70 75 80
 Phe Ala Leu Leu Ile Val Phe Phe Ser Asn Ala Leu Leu Ala Gln Asp
 85 90 95
 Leu Lys Ile Ala Ala Ala Asn Leu Thr Arg Ala Leu Lys Ala Leu
 100 105 110
 Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp Ala Ile Asn Ile Ser
 115 120 125
 Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile Ala Gln Asn Ala Pro
 130 135 140
 Phe Asp Leu Phe Ile Ser Ala Asp Ile Ala Arg Pro Lys Lys Leu Tyr

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1202

```

145          150          155          160
Asp Glu Lys Ile Thr Pro Phe Lys Glu Glu Val Tyr Ala Lys Gly Val
          165          170          175
Leu Val Leu Trp Ser Glu Asn Leu Lys Met Asp Ser Leu Glu Ile Leu
          180          185          190
Lys Asp Pro Lys Ile Lys Arg Ile Ala Met Ala Asn Pro Lys Leu Ala
          195          200          205
Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Asp Arg Leu Lys Leu Thr
          210          215          220
Pro Ser Leu Lys Ser Lys Ile Ile Tyr Gly Ala Ser Ile Ser Gln Ala
          225          230          235          240
His Gln Phe Ile Ala Thr Lys Asn Ala Gln Ile Gly Phe Gly Ala Leu
          245          250          255
Ser Leu Ile Asp Lys Lys Asp Lys Asn Leu Ser Tyr Phe Ile Ile Asp
          260          265          270
Lys Thr Leu Tyr Asn Pro Ile Glu Gln Ala Leu Ile Ile Thr Lys Asn
          275          280          285
Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys Asp Phe Leu Phe Ser
          290          295          300
Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly Tyr Ile Val Asp
          305          310          315

```

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658

```

Lys Arg Arg Thr Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser
1          5          10          15
Phe Ser Leu Ala Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile
          20          25          30
Phe Leu Gly Tyr Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu
          35          40          45
Thr Glu Thr Leu Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu
          50          55          60
Gly Phe Tyr Leu Leu Leu Ile Phe Ser Pro Ser Phe Leu Gly Ala
          65          70          75          80
Phe Leu Gln Asp Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly
          85          90          95
Leu Ile Leu Gly Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro
          100          105          110
Ile Lys Ser Ala Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser
          115          120          125
Tyr Ser Leu Gly Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu
          130          135          140
Pro Asn Ile Lys Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met
          145          150          155          160
His Thr Ile Gly Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile
          165          170          175

```

SUBSTITUTE SHEET (RULE 26)

1203

Leu Gly Glu Thr Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu
 180 185 190
 Ala Leu Asn Tyr Ser Lys Ala His Gln Tyr Ala Leu Thr Leu Thr Leu
 195 200 205
 Ile Ser Phe Ser Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln
 210 215 220
 Ser Ser Phe Leu
 225

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659

Asn Phe Ile Phe Gly Glu Phe Ile Met Lys Arg Ser Ser Val Phe Ser
 1 5 10 15
 Phe Leu Val Ala Phe Leu Leu Val Val Gly Cys Ser His Lys Met Asp
 20 25 30
 Asn Lys Thr Val Ala Gly Asp Val Ser Thr Lys Ala Val Gln Thr Ala
 35 40 45
 Pro Val Thr Thr Glu Pro Ala Pro Glu Lys Glu Glu Pro Lys Gln Glu
 50 55 60
 Pro Ala Pro Val Val Glu Glu Lys Pro Ala Ile Glu Ser Gly Thr Ile
 65 70 75 80
 Ile Ala Ser Ile Tyr Phe Asp Phe Asp Lys Tyr Glu Ile Lys Glu Ser
 85 90 95
 Asp Gln Glu Thr Leu Asp Glu Ile Val Gln Lys Ala Lys Glu Asn His
 100 105 110
 Met Gln Val Leu Leu Glu Gly Asn Thr Asp Glu Phe Gly Ser Ser Glu
 115 120 125
 Tyr Asn Gln Ala Leu Gly Val Lys Arg Thr Leu Ser Val Lys Asn Ala
 130 135 140
 Leu Val Ile Lys Gly Val Glu Lys Asp Met Ile Lys Thr Ile Ser Phe
 145 150 155 160
 Gly Glu Ser Lys Pro Lys Cys Val Gln Lys Thr Arg Glu Cys Tyr Arg
 165 170 175
 Glu Asn Arg Arg Val Asp Val Lys Leu Val Lys
 180 185

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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1204

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660

```

Lys Arg Ile Lys Arg Gly Phe Phe Met Gln Glu Ala Leu Leu Arg Phe
1          5          10          15
Gln Glu Gly Phe Lys Glu Trp Gly Tyr Leu Ile Leu Phe Leu Tyr Ser
20          25          30
Leu Gly Gly Gly Tyr Val Gly Ile Val Ile Ala Ser Ile Leu Ser Ala
35          40          45
Thr Thr His Ala Leu Asp Ile Lys Ile Thr Ile Leu Val Ala Phe Leu
50          55          60
Gly Asn Leu Ile Gly Ser Gly Ala Leu Val Ile Phe Ala Arg Tyr Gln
65          70          75          80
Lys Arg Glu Phe Leu Lys Tyr Phe Gln Lys His Arg Arg Lys Leu Ala
85          90          95
Leu Ala Ser Leu Trp Val Lys Arg Tyr Ala Leu Leu Met Ile Phe Val
100          105          110
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Ile Gly
115          120          125
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
130          135          140
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
145          150          155          160
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
165          170          175
Phe Val Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
180          185          190
Lys Arg Tyr Ser Arg Lys Met Gly Phe
195          200

```

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661

```

Ala Ser Phe Asn Tyr Asn Phe Gln Met Leu Arg Lys Asn Ile Leu Ala
1          5          10          15
Tyr Tyr Gly Ala Asn Phe Leu Leu Ile Ile Ala Gln Ser Leu Pro His
20          25          30
Ala Ile Leu Thr Pro Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu
35          40          45

```

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```

Ile Leu Leu Val Gln Thr Phe Phe Ser Phe Cys Val Leu Val Ala Glu
50          55          60
Tyr Pro Ser Gly Val Leu Ala Asp Leu Met Ser Arg Lys Asn Leu Phe
65          70          75          80
Leu Val Ser Asn Val Phe Leu Ile Ala Ser Phe Ser Phe Val Leu Phe
85          90          95
Phe Asp Ser Phe Ile Leu Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu
100        105        110
Tyr Ser Ala Cys Ser Ser Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp
115        120        125
Ile Lys Glu Asn Lys Lys Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn
130        135        140
Gln Ile Thr Tyr Leu Gly Met Ile Ile Gly Ser Ser Leu Gly Ser Phe
145        150        155        160
Leu Tyr Leu Lys Val His Ala Met Leu Tyr Val Val Gly Ile Phe Leu
165        170        175
Ile Met Leu Cys Ala Leu Thr Ile Ile Ile Tyr Phe Lys Glu Lys Glu
180        185        190
Gly Asp Phe Lys Ser Gln Lys Asn Leu Lys Leu Lys Glu Gln Val
195        200        205
Lys Gly Ser Leu Lys Glu Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu
210        215        220
Leu Val Gly His Leu Ile Thr Pro Val Phe Phe Met Ser His Phe Gln
225        230        235        240
Met Trp Gln Ala Tyr Phe Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu
245        250        255
Phe Val Phe Tyr Ile Ala Phe Gln Val Ile Ser Ile Leu Ile His Phe
260        265        270
Leu Lys Ala Lys Asn Tyr Ser Gln Lys Ile Ala Leu Ser Ser Leu Leu
275        280        285
Val Leu Leu Gly Val Ser Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys
290        295        300
Phe Ile Gly Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser
305        310        315        320
Tyr Cys Leu Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile
325        330        335
Ser Ser Leu Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val
340        345        350
Leu Ile Leu Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu
355        360        365
Thr Ile Ile Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe
370        375        380
Phe Leu Tyr Lys Ala Lys Pro Phe Asp Glu
385        390

```

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662

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```

Arg Arg Asn Leu Thr Arg Gln His Gly Ser Val Lys Lys Arg Glu Lys
1      5      10      15
Arg Phe Lys Thr His Ala Ser Leu Cys Asp Ser Val Arg Ser Gly Lys
      20      25      30
Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp Ile Val Asn Ile Gly
      35      40      45
Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val Cys Thr Ala Leu Lys
      50      55      60
Arg Tyr Gly His Pro Arg Leu Glu Met His Phe Val Ser Asn Val Asp
65      70      75      80
Gly Thr Gln Ile Leu Asp Val
      85

```

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663

```

Gln His Tyr Pro Asn Asn Leu Lys Asp Ile Glu Met Asn Thr Glu Ile
1      5      10      15
Leu Thr Ile Met Leu Val Val Ser Val Leu Met Gly Leu Val Gly Leu
      20      25      30
Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln Phe Asp Asp Glu Lys
      35      40      45
Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Ala Ser Asp Leu Asn Glu
      50      55      60
Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn
65      70

```

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664

```

Glu Met Gln Phe Leu His Ala His Leu Leu Ser Val Val Ile Phe Phe
1      5      10      15
Pro Met Leu Ser Ala Leu Leu Ala Phe Phe Met Ser Asp Gln Ala Ser
      20      25      30
Arg Ala Tyr Ala Ile Val Ile Ala Leu Ile Glu Leu Leu Val Leu
      35      40      45
Leu Leu Trp His Gly Phe Asp Ile Gln Thr Ala Gly Met Gln Phe Glu
      50      55      60
Glu Met Lys Glu Leu Ala Tyr Gln Ile Gly Val Asn Tyr His Val Gly
      65      70      75      80
Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn Ala Ile Val Val
      85      90      95
Leu Leu Ser Val Ile Tyr Val Lys Glu Arg Arg Lys Asp Phe Val Ile
      100      105      110
Cys Leu Leu Leu Glu Gly Ile Leu Met Gly Val Phe Ser Ser Leu
      115      120      125
Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser Leu Leu Pro Val
      130      135      140
Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys Ile Tyr Ser Gly
      145      150      155      160
Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu Cys Met Leu Leu
      165      170      175
Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn Tyr Gly Met Met
      180      185      190
Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe Ser Ser Gly Ile
      195      200      205
Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile Ala Val Lys Ile
      210      215      220
Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg Ile Leu Thr Pro
      225      230      235      240
Pro Leu

```

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665

```

Lys Arg Ser Leu Met Leu Ile Asp Ile Leu His Ile Ser Phe Asp Ser
1      5      10      15
Phe Ser Phe Glu Ser Ile Leu Pro Met Leu Val Leu Val Cys Gly Gly
      20      25      30
Ile Phe Thr Leu Leu Ile Asn Ala Phe Thr Ser Arg Phe Ser Arg Asn
      35      40      45
Leu Asn Val Phe Leu Cys Met Leu Phe Leu Val Leu Asp Phe Leu Val
      50      55      60
Val Ser Gly Leu Glu Glu Gln Glu Asn Ala Phe Phe Gly Phe Leu Ser

```

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```

65      70      75      80
Leu Asp Thr Leu Ser Leu Ile Ser Gln Ser Ile Val Leu Ile Ser Ala
      85      90      95
Phe Phe Leu Ile Phe Leu Ala Leu Ser Lys Glu Arg Phe Asn Glu Phe
      100     105     110
Gln Thr Ala Glu Phe Tyr Ser Leu Tyr Leu Phe Ile Val Ala Gly Phe
      115     120     125
Gln Phe Met Val Ser Ser Asn Gln Phe Val Val Ile Leu Ile Gly Leu
      130     135     140
Glu Thr Ala Pro Leu Pro Leu Cys Val Leu Met Ala Leu Ser Asp Lys
      145     150     155     160
Arg Tyr Gly Leu Glu Ala Gly Ile Lys Tyr Phe Thr Met Gly Ala Met
      165     170     175
Ala Ser Ala Phe Phe Ala Met Gly Ala Met Ala Phe Tyr Leu Leu Thr
      180     185     190
Gly Ser Leu Asn Leu Glu Val Ile Thr Leu Tyr Leu His Thr Glu Gly
      195     200     205
Ile Thr Asn Pro Met Leu Phe Ala Met Gly Thr Ile Phe Leu Ile Gly
      210     215     220
Ala Ile Gly Phe Lys Val Ser Leu Val Pro Phe His Thr Trp Met Pro
      225     230     235     240
Asp Val Tyr Glu Gly Asn Asn Pro Val Phe Ala Ser Tyr Ile Ser Ile
      245     250     255
Val Pro Lys Ile Ala Gly Phe Val Val Ala Thr Arg Leu Phe Gly Ala
      260     265     270
Phe Ile Asp Thr His Thr Ala Trp Val Glu Asp Ile Phe Tyr Val Leu
      275     280     285
Ile Leu Met Thr Ile Thr Ile Pro Asn Phe Ile Ala Leu Trp Gln Glu
      290     295     300
Asp Val Lys Arg Met Leu Ala Tyr Ser Ser Ile Ser His Ser Gly Phe
      305     310     315     320
Ala Leu Ala Cys Val Phe Ile His Thr Glu Asp Ser Gln Gln Ala Met
      325     330     335
Phe Val Tyr Trp Phe Met Phe Ala Phe Thr Tyr Ile Gly Ala Phe Gly
      340     345     350
Leu Leu Trp Leu Leu Lys Ser Arg Glu Lys Thr Trp Asp Glu Arg Tyr
      355     360     365
Asp His Pro Tyr Ser Lys Phe Asn Gly Leu Ile Lys Thr His Pro Leu
      370     375     380
Val Ala Ile Leu Gly Ala Ile Phe Val Phe Gly Leu Ala Gly Ile Pro
      385     390     395     400
Pro Phe Ser Val Phe Trp Gly Lys Phe Leu Ala Val Glu Ser Ala Leu
      405     410     415
Glu Ser Asn His Ile Leu Leu Ala Val Val Met Leu Val Asn Ser Ala
      420     425     430
Val Ala Ala Phe Tyr Tyr Phe Arg Trp Leu Val Ala Met Phe Phe Asn
      435     440     445
Lys Pro Leu Gln Thr Gln Ser Tyr Ala Gln Asn Asp Ile Tyr Thr Gln
      450     455     460
Asn Ala Thr Met Pro Ile Tyr Ala Val Ile Ile Ala Met Ala Leu Ala
      465     470     475     480
Cys Leu Phe Ser Val Phe Met Met Arg Gly Leu Leu Glu Phe Val Ala
      485     490     495

```

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666

```

Asn Pro Ala Leu Ser Leu His Thr Trp Leu Pro Tyr Ala Tyr Ser Asn
1      5      10      15
Ala Pro Thr Leu Gly Ser Val Met Leu Ser Ala Leu Leu Ser Lys Met
20      25      30
Gly Thr Tyr Ala Leu Leu Arg Phe Leu Leu Pro Leu Phe Pro Glu Leu
35      40      45
Ser Glu Ile Tyr Leu Thr Pro Ile Ala Ile Val Ala Leu Cys Met Ile
50      55      60
Ile Tyr Gly Gly Phe Leu Ala Tyr Ala Gln Lys Asp Leu Lys Thr Leu
65      70      75      80
Ile Ala Tyr Ser Ser Phe Ser His Met Gly Val Val Val Leu Gly Val
85      90      95
Phe Ser Phe Asn Val Glu Gly Val Ser Gly Ala Val Phe Met Met Phe
100     105     110
Ala His Gly Val Ile Val Met Gly Leu Phe Leu Leu Ala Gly Ile Leu
115     120     125
Glu Glu Arg Ala Ser Ser Leu Glu Ile Ala Arg Phe Gly Ser Ile Ala
130     135     140
Lys Ser Ala Pro Val Phe Ala Ala Phe Phe Met Ile Val Leu Met Ala
145     150     155     160
Asn Val Gly Met Pro Leu Ser Ile Gly Phe Val Gly Glu Phe Leu Ser
165     170     175
Leu Leu Gly Phe Phe Ala Thr Tyr Pro Leu Leu Ala Ile Ile Ala Gly
180     185     190
Thr Ser Ile Ile Leu Ser Ala Val Tyr Met Leu Thr Ser Tyr Lys Asp
195     200     205
Val Phe Phe Gly Asn Leu Lys Thr Gly Asn Asn Gln Ile Ser Val Phe
210     215     220
Glu Asp Leu Asn Ala Arg Glu Val Gly Val Leu Ser Val Ile Leu Ala
225     230     235     240
Leu Ile Leu Ile Leu Gly Ile Tyr Pro Lys Ala Leu Leu Lys Pro Ile
245     250     255
Glu Gln Gly Phe Lys Gln Leu Leu Glu Val Ile Glu Ile Arg Ser Leu
260     265     270
Leu Phe Leu Gly Ser Leu Asp Thr Lys Ile Lys Glu Val Ser Tyr Val
275     280     285
Asn Arg Tyr Ser Pro His Leu Phe
290     295

```

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667

```

Ile Tyr Ser Lys Thr Arg Ser His Asp Met Asp Ile Ser Ile Phe Arg
1      5      10      15
Glu Tyr Asp Ile Arg Gly Ile Tyr Pro Thr Thr Leu Asp Glu Asn Thr
20     25     30
Ala Phe Ser Ile Gly Val Glu Leu Gly Lys Ile Met Arg Glu Tyr Asp
35     40     45
Lys Ser Val Phe Val Gly His Asp Ala Arg Val His Gly Arg Phe Leu
50     55     60
Phe Glu Val Leu Ser Ala Gly Leu Gln Ser Ser Gly Leu Lys Val Tyr
65     70     75     80
Asp Leu Gly Leu Ile Pro Thr Pro Val Ala Tyr Phe Ala Ala Phe Asn
85     90     95
Glu Ile Asp Asn Ile Gln Cys Pro Asn Ser Ile Met Ile Thr Gly Ser
100    105    110
His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile Thr Leu Asn Gln Asn
115    120    125
Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys Asn Thr Leu Leu Asn
130    135    140
Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr Pro Glu Lys Val Asn
145    150    155    160
Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys Asp Phe Lys His Leu
165    170    175
Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe Gly Asn Gly Val Gly
180    185    190
Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu Asn Ile Asp Phe Ser
195    200    205
Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro Asn His His Pro Asp
210    215    220
Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu Lys His Met Arg Glu
225    230    235    240
Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Ile
245    250    255
Ala Met Leu Ser Ser His His Ile Tyr Ala Gly Asp Glu Leu Ala Ile
260    265    270
Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile Thr Pro Phe Val Ile
275    280    285
Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn Ala Ile Asn Thr Phe
290    295    300
Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser Asn Leu Lys Ile Lys
305    310    315    320
Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu Met Ser Gly His Ile
325    330    335
Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp Ala Leu Tyr Ala Cys
340    345    350
Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser Pro Ser Asp Leu Glu
355    360    365
Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr Thr Pro Glu Glu Lys
370    375    380
Ile Ala Val Ser Glu Glu Lys Phe Glu Ile Ile Arg Asn Leu Gln
385    390    395    400
Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro Thr Ile Lys Glu Ile
405    410    415
Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu His Gly Phe Gly Leu
420    425    430
Ile Arg Ala Ser Asn Thr Thr Pro Tyr Leu Val Ser Arg Phe Glu Gly
435    440    445
Lys Asp Glu Thr Thr Ala Leu Glu Tyr Lys Arg Ala Leu Leu Gly Leu
450    455    460
Leu Glu Lys Leu
465

```

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(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668

```

Gly Ile Phe Met Asn Glu Ile Ile Leu Ile Thr Gly Ala Tyr Gly Met
1           5           10           15
Val Gly Gln Asn Thr Ala Leu Tyr Phe Lys Lys Asn Lys Pro Asp Val
          20           25           30
Thr Leu Leu Thr Pro Lys Lys Ser Glu Leu Tyr Leu Leu Asp Lys Asp
          35           40           45
Asn Val Gln Ala Tyr Leu Lys Glu Tyr Lys Pro Thr Gly Ile Ile His
          50           55           60
Cys Ala Gly Arg Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser
65          70          75          80
Thr Tyr Met Val Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser
          85          90          95
Ala Leu Asp Leu Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys
          100         105         110
Ala Tyr Pro Lys Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu
          115         120         125
Asn Gly Ser Leu Glu Pro Thr Asn Glu Gly Tyr Ala Leu Ala Lys Leu
          130         135         140
Ser Val Met Lys Tyr Cys Glu Tyr Val Ser Ala Glu Lys Gly Val Phe
145         150         155         160
Tyr Lys Thr Leu Val Pro Cys Asn Leu Tyr Gly Glu Phe Asp Lys Phe
          165         170         175
Glu Glu Lys Ile Ala His Met Ile Pro Gly Leu Ile Ala Arg Met His
          180         185         190
Thr Ala Lys Leu Lys Asn Glu Lys Asn Phe Ala Met Trp Gly Asp Gly
          195         200         205
Thr Ala Glu Glu Ser Ile
210

```

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669

```

Ala His Ala Asn Arg Thr Ile Ile His Arg Ile Asp Asp Ser Ile Ala
1      5      10      15
Gln Arg Val Asp Asn Ala Ile Arg Pro Met Arg Leu Val Arg Gly Phe
      20      25      30
Ala Pro Leu Tyr Leu Thr Leu Pro Lys Arg Ser Phe Asn Ala Pro Lys
      35      40      45
Lys Ile Leu Ala Leu Gly Ala Glu Gln Lys Gly His Phe Ser Leu Leu
50      55      60
Asp Ser Glu Thr Ser Val Leu Leu Leu Ser Pro Phe Cys Gly Asp Leu
65      70      75      80
Ser Val Leu Glu Asn Glu Lys His Phe Lys Glu Thr Leu Asn Phe Phe
      85      90      95
Leu Lys Thr Tyr Asp Phe Lys Pro Thr Leu Leu Ala Cys Asp Glu His
      100      105      110
Gln Asn Tyr Thr Thr Thr Lys Met Ala Phe Asp Phe Asn Thr Pro Leu
      115      120      125
Leu Gln Val Gln His His His Ala His Phe Leu Ala Ser Val Leu Asp
130      135      140
Ala Leu Leu Gln Asp Pro His Leu Asn His Pro Phe Ile Gly Ile Val
145      150      155      160
Trp Asp Gly Ser Gly Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys
      165      170      175
Phe Val Gly Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu
180      185      190
Phe Trp Leu Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu
195      200      205
Val Leu Glu Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg
210      215      220
Val Gln Lys His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met
225      230      235      240
His Asp Lys Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu
      245      250      255
Phe Asp Ile Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe
260      265      270
Glu Ala Glu Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp
275      280      285
Glu Ile Ala Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu
290      295      300
Lys Glu Phe Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro
305      310      315      320
Lys Arg Ile Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr
      325      330      335
Ala Leu Ile Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly
340      345      350
Val Phe Cys Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys
355      360      365
Lys Leu Gln Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp
370      375      380
Ser Ser Ile Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr
385      390      395      400
Ile Ile Lys Lys Gly
      405

```

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670

```

Arg Phe Glu Cys Gly Ala Ser Asp Met Ser Gly Trp Leu Leu Met Gly
1      5      10      15
Leu Pro Gly Ala Leu Tyr Val Gly Gly Leu Ile Asn Ser His Ile Ala
20     25     30
Ile Gly Leu Ser Leu Gly Ala Leu Ile Asn Trp Val Phe Val Ala Lys
35     40     45
Arg Leu Arg Ile Tyr Thr Ser Val Ile Ala Asn Ser Ile Thr Ile Ser
50     55     60
Asp Tyr Phe Glu Thr Arg Phe Ser Asp Asp Lys His Ile Leu Arg Leu
65     70     75     80
Ile Ser Ala Phe Val Ile Leu Ile Leu Lys Ile Phe Tyr Phe Ser Ser
85     90     95
Gly Leu Val Ser Gly Ala Lys Leu Phe Glu Pro Thr Phe Gly Ile Gln
100    105    110
Tyr Thr Tyr Ala Leu Ser Ile Gly Thr Leu Ile Ile Val Ser Tyr Thr
115    120    125
Phe Leu Gly Arg Tyr Lys Ala Val Cys Trp Thr Asp Leu Ile Gln Gly
130    135    140
Leu Leu Met Met Ser Ala Leu Ile Val Val Pro Ile Val Met Ile Ile
145    150    155    160
His Leu Gly Gly Ile Gly Glu Gly Ile Lys Ile Ile Lys Glu Ile Lys
165    170    175
Pro Glu Asn Leu Ser Phe Leu Gln Gly Ser Ser Val Val Ala Ile Ile
180    185    190
Ser Ser Leu Ala Trp Gly Leu Gly Tyr Phe Gly Gln Pro His Ile Leu
195    200    205
Val Arg Phe Met Ser Ile Arg Ser Ile Arg Asp Val Pro Lys Ala Thr
210    215    220
Thr Ile Gly Ile Ser Trp Met Val Ile Ser Leu Ile Gly Ala Cys Val
225    230    235    240
Met Gly Leu Leu Gly Val Ala Tyr Val His Lys Phe Asp Leu Ser Leu
245    250    255
Glu Asp Pro Glu Lys Ile Phe Ile Val Met Ser Gln Leu Leu Phe Asn
260    265    270
Pro Trp Ile Thr Gly Ile Leu Leu Ser Ala Ile Leu Ala Ala Val Met
275    280    285
Ser Thr Ala Ser Ser Gln Leu Leu Val Ser Ser Ser Thr Ile Ala Glu
290    295    300
Asp Phe Tyr Ala Thr Ile Phe Asn Lys Asn Ala Pro Gln Lys Leu Val
305    310    315    320
Met Thr Ile Ser Arg Leu Ser Val Leu Gly Val Ala Cys Ile Ala Phe
325    330    335
Phe Ile Ser Thr Asp Lys Asn Ala Ser Ile Leu Ser Ile Val Ser Tyr
340    345    350
Ala Trp Ala Gly Phe Gly Ala Ser Phe Gly Ser Val Ile Leu Phe Ser
355    360    365
Leu Phe Trp Ser Arg Met Thr Arg Ile Gly Ala Ile Ala Gly Met Leu
370    375    380
Ser Gly Ala Ser Thr Val Ile Leu Tyr Asp Lys Phe Gly Lys Ser Phe

```

SUBSTITUTE SHEET (RULE 26)

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```

385          390          395          400
Leu Asp Ile Tyr Glu Ile Val Pro Gly Phe Ile Val Ala Ser Val Ala
          405          410          415
Ile Val Ala Phe Ser Leu Phe Ser Ser Val Arg Ser Gly Thr Lys Glu
          420          425          430
Ala Phe Glu Thr Met Leu Lys Glu Ile Glu Ser Leu Lys His
          435          440          445

```

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671

```

Asn Lys Trp Ile Lys Gly Ala Val Val Phe Val Gly Gly Phe Ala Thr
1          5          10          15
Ile Thr Thr Phe Ser Leu Ile Tyr His Gln Lys Pro Lys Ala Pro Leu
          20          25          30
Asn Asn Gln Pro Ser Leu Leu Asn Asp Asp Glu Val Lys Tyr Pro Leu
          35          40          45
Gln Asp Tyr Thr Phe Thr Gln Asn Pro Gln Pro Thr Asn Thr Glu Ser
50          55          60
Ser Lys Asp Ala Thr Ile Lys Ala Leu Gln Glu Gln Leu Lys Ala Ala
65          70          75          80
Leu Lys Ala Leu Asn Ser Lys Glu Met Asn Tyr Ser Lys Glu Glu Thr
          85          90          95
Phe Thr Ser Pro Pro Met Asp Pro Lys Thr Thr Pro Pro Lys Lys Asp
          100          105          110
Phe Ser Pro Lys Gln Leu Asp Leu Leu Ala Ser Arg Ile Thr Pro Phe
          115          120          125
Lys Gln Ser Pro Lys Asn Tyr Glu Glu Asn Leu Ile Phe Pro Val Asp
130          135          140
Asn Pro Asn Gly Ile Asp Ser Phe Thr Asn Leu Lys Glu Lys Asp Ile
145          150          155          160
Ala Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met
          165          170          175
Ile Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys
          180          185          190
Val Ile Ala Gln Val Glu Ser Asp Ile Phe Ala Ser Met Gly Lys Ala
          195          200          205
Val Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn
210          215          220
Asn Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile
225          230          235          240
Thr Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp
          245          250          255
Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe
          260          265          270
Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu
          275          280          285

```

SUBSTITUTE SHEET (RULE 26)

1215

```

Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Glu
 290                               295                               300
Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu Leu Gln Leu Met Arg Gln
305                               310                               315                               320
Ser Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys
                               325                               330                               335
Ser Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe
                               340                               345                               350
Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu
                               355                               360                               365
Val Ile Ala Glu Phe Leu Lys
 370                               375

```

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672

```

Lys Ala Ala Phe Cys Ile Gly Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe
 1                               5                               10                               15
Leu Asp Glu Phe Leu Ile Lys Leu Tyr Leu Gln Pro Ser Glu Gln Asp
 20                               25                               30
Ala Leu Phe Met Gln Glu Thr Lys Arg Ala Met Asn Ile Tyr Tyr Val
 35                               40                               45
Gly Tyr Val Phe Leu Gly Met Thr Leu Leu Cys Ala Val Phe Phe Gln
 50                               55                               60
Ser Ile Gln Arg Thr Lys Ser Ser Phe Ile Ile Thr Ile Ser His Thr
 65                               70                               75                               80
Leu Gly Phe Ile Val Ile Leu Leu Pro Ile Leu Ser His Phe Tyr Gly
 85                               90                               95
Val Asn Gly Ile Trp Val Thr Tyr Pro Ile Ala Gln Phe Leu Ala Val
 100                               105                               110
Phe Gly Ser Val Arg Gly Asn Leu Leu
 115                               120

```

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673

```

Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1           5           10           15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
          20           25           30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
          35           40           45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
50           55           60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65           70           75           80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
          85           90           95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
          100          105          110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Arg Phe Leu Gly Ala Met Thr
          115          120          125
Leu Tyr
130

```

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674

```

Asn His Phe Asn Gly Cys Val Phe Arg Val Gln His Leu Leu Ala Asp
1           5           10           15
Val Phe Val Val Asn Asp Lys Arg Pro Val Leu Ala Met Val Ala Met
          20           25           30
Leu Ile Gly Ser Leu Ala Asn Ile Phe Phe Asn Tyr Leu Phe Ile Phe
          35           40           45
Val Leu Glu Val Gly Val Gln Gly Ser Ala Ile Ala Thr Val Ile Gly
50           55           60
His Ala Ile Gly Val Leu Val Leu Met Gln His Phe Trp Arg Lys Lys
65           70           75           80
Gly Gln Leu Tyr Phe Ile Lys Arg Phe Ser Leu Ser Ser Val Ile Ser
          85           90           95
Ser Ala Lys Ser Gly Val Pro Gln Ser Thr Ala Glu Phe Ser Ala Ser
          100          105          110
Ile Met Ile Leu Leu Phe Asn Thr Ala Ile Met His Thr Ala Gly Glu
          115          120          125
Arg Phe Val Ser Met Tyr Gly Ile Val Met Tyr Asn Ala Ile Ile Phe
          130          135          140

```

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Phe Thr Thr Leu Phe Ala Ile Ser Gln Gly Ile Gln Pro Ile Ala Glu
 145 150 155 160
 Leu

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675

Phe Leu Asn Ile Arg Asp Leu Thr Met Ile Phe Ser Ser Leu Phe Ser
 1 5 10 15
 Val Val Gly Met Ala Val Leu Phe Leu Ile Ala Trp Val Phe Ser Gly
 20 25 30
 Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser Ala Phe Val Ile
 35 40 45
 Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro Leu Gly Arg Glu
 50 55 60
 Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val Ile Gly Tyr Gly
 65 70 75 80
 Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala Pro Asn Ala Lys
 85 90 95
 Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile Asn Val Leu Ala
 100 105 110
 Ile Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu Tyr Tyr Leu Lys
 115 120 125
 Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala Leu Gln Lys Cys
 130 135 140
 Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala Asn Ile Phe
 145 150 155 160
 Val Ala His Thr Glu Ala Pro Leu Val Ile Lys Pro Tyr Leu Lys Ser
 165 170 175
 Met Ser Asp Ser Glu Ile Phe Ala Val Met Cys Val Gly Met Ala Ser
 180 185 190
 Val Ala Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro Leu
 195 200 205
 Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu Leu
 210 215 220
 Phe Ala Lys Ile Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His Ala
 225 230 235 240
 Asp Val Ser Ala Glu His Val Asn Ile Ile Glu Ala Ile Ala Asn
 245 250 255
 Gly Ala Ser Thr Gly Leu His Leu Ala Leu His Val Gly Ala Met Leu
 260 265 270
 Leu Ala Phe Val Gly Met Leu Ala Leu Val Asn Gly Leu Leu Gly Val
 275 280 285
 Val Gly Gly Phe Leu Gly Met Glu His Leu Ser Leu Gly Val Val Leu
 290 295 300
 Gly Thr Leu Leu Lys Pro Leu Ala Phe Met Leu Gly Val Pro Trp Ser

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```

305          310          315          320
Gln Ala Gly Ile Ala Gly Glu Ile Ile Gly Ile Lys Ile Ala Leu Asn
          325          330          335
Glu Phe Val Gly Tyr Met Gln Leu Leu Pro Tyr Leu Gly Asp Asn Pro
          340          345          350
Pro Leu Ile Leu Ser Glu Lys Thr Lys Ala Ile Ile Thr Phe Ala Leu
          355          360          365
Cys Gly Phe Ala Asn Leu Ser Ser Val Ala Met Leu Ile Gly Gly Leu
          370          375          380
Gly Ser Leu Val Pro Lys Lys Lys Asp Phe Ile Ala Arg Leu Ala Leu
385          390          395          400
Lys Ala Val Leu Val Gly Thr Leu Ser Asn Phe Met Ser Ala Thr Ile
          405          410          415
Ala Gly Leu Phe Ile Gly Leu Ser Ala Asn
          420          425

```

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676

```

Thr Leu Ser Lys Glu Glu Gly Leu Met Pro Gln Asn Gln Leu Val Ile
1          5          10          15
Thr Ile Ile Asp Glu Ser Gly Ser Lys Gln Leu Lys Phe Ser Lys Asn
          20          25          30
Leu Lys Arg Asn Leu Ile Ile Ser Val Val Ile Leu Leu Leu Ile Val
          35          40          45
Gly Leu Gly Val Gly Phe Leu Lys Phe Leu Ile Ala Lys Met Asp Thr
          50          55          60
Met Thr Ser Glu Arg Asn Ala Val Leu Arg Asp Phe Arg Gly Leu Tyr
65          70          75          80
Gln Lys Asn Tyr Ala Leu Ala Lys Glu Ile Lys Asn Lys Arg Glu Glu
          85          90          95
Leu Phe Ile Val Gly Gln Lys Ile Arg Gly Leu Glu Ser Leu Ile Glu
          100          105          110
Ile Lys Lys Gly Ala Asn Gly Gly Gly His Leu Tyr Asp Glu Val Asp
          115          120          125
Leu Glu Asn Leu Ser Leu Asn Gln Lys His Leu Ala Leu Met Leu Ile
          130          135          140
Pro Asn Gly Met Pro Leu Lys Thr Tyr Ser Ala Ile Lys Pro Thr Lys
145          150          155          160
Glu Arg Asn His Pro Ile Lys Lys Ile Lys Gly Val Glu Ser Gly Ile
          165          170          175
Asp Phe Ile Ala Pro Leu Asn Thr Pro Val Tyr Ala Ser Ala Asp Gly
          180          185          190
Ile Val Asp Phe Val Lys Thr Arg Ser Asn Ala Gly Tyr Gly Asn Leu
          195          200          205
Val Arg Ile Glu His Ala Phe Gly Phe Ser Ser Ile Tyr Thr His Leu
210          215          220

```

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```

Asp His Val Asn Val Gln Pro Lys Ser Phe Ile Gln Lys Gly Gln Leu
225                230                235                240
Ile Gly Tyr Ser Gly Lys Ser Gly Asn Ser Gly Gly Glu Lys Leu His
                245                250                255
Tyr Glu Val Arg Phe Leu Gly Lys Ile Leu Asp Ala Glu Lys Phe Leu
                260                265                270
Ala Trp Asp Leu Asp His Phe Gln Ser Ala Leu Glu Glu Asn Lys Phe
                275                280                285
Ile Glu Trp Lys Asn Leu Phe Trp Val Leu Glu Asp Ile Val Gln Leu
                290                295                300
Gln Glu His Val Asp Lys Asp Thr Leu Lys Gly Gln
305                310                315

```

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677

```

Gly Phe Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp
1                5                10                15
Ser Lys Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile
                20                25                30
Ser Leu Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly
                35                40                45
Val Ser Leu Leu Val Leu Asn Lys Lys Glu Ile Lys Asn Ile Glu Lys Gln
                50                55                60
His Ala Leu Ile Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu
                65                70                75                80
Lys Leu Ser Leu Gln Met Asp Glu Phe Leu Asp Asp Leu Gln Leu Ser
                85                90                95
Gly Glu Arg Ile Asn Asp Leu Glu Glu Val Val Gly Val Asn Arg Pro
                100                105                110
Glu Glu Glu Lys Glu Glu Gly Asn Phe Ser Ser Arg Leu Asp Val Ala
                115                120                125
Gly Ile Thr Gly Leu Gln Lys Ser Phe Ile Met Arg Leu Ile Pro Asn
                130                135                140
Asp Tyr Pro Leu Glu Ser Tyr Arg Arg Val Ser Ala Ala Phe Asn Lys
                145                150                155                160
Arg Met His Pro Ile Leu His Val Leu His Asn His Thr Gly Leu Asp
                165                170                175
Leu Ser Thr Ala Ile Asn Thr Pro Val Tyr Ala Ser Ala Ser Gly Val
                180                185                190
Val Gly Leu Ala Ser Lys Gly Trp Asn Gly Gly Tyr Gly Asn Leu Ile
                195                200                205
Lys Val Phe His Pro Phe Gly Phe Lys Thr Tyr Tyr Ala His Leu Asn
                210                215                220
Lys Ile Val Val Lys Thr Gly Glu Phe Val Lys Lys Gly Gln Leu Ile
                225                230                235                240
Gly Tyr Ser Gly Asn Thr Gly Met Ser Thr Gly Pro His Leu His Tyr

```

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| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | | | | | 245 | | | | | 250 | | | | | 255 | | | | |
| Glu | Val | Arg | Phe | Leu | Asp | Gln | Pro | Ile | Asn | Pro | Met | Ser | Phe | Thr | Lys | | | | |
| | | | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Trp | Asn | Met | Lys | Asp | Phe | Glu | Glu | Val | Phe | Asn | Lys | Glu | Arg | Ser | Ile | | | | |
| | | | | | 275 | | | | | 280 | | | | | 285 | | | | |
| Arg | Trp | Gln | Ser | Leu | Ile | Thr | Ile | Ile | Asn | Arg | Leu | Met | Gln | Lys | Gln | | | | |
| | | | | | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Gln | Arg | Leu | Ser | Ser | Leu | Lys | Ala | Pro | Lys | | | | | | | | | |
| | | | | | 305 | | | | | 310 | | | | | 315 | | | | |

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature

(B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1678

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | Ile | Glu | Phe | Ala | Asn | Leu | Tyr | His | Ile | Pro | Ile | Lys | Val | Ile | Thr |
| Gln | Ser | Pro | Gln | Asn | Leu | Pro | His | Thr | Lys | Glu | Glu | Ile | Leu | Lys | Asn |
| Ser | Gly | Glu | Trp | Ser | Asp | Leu | Ser | Ser | Ser | Leu | Ala | Arg | Lys | Lys | Ile |
| Leu | Pro | Tyr | Phe | Asp | Lys | Glu | Asn | Leu | Gly | Lys | Arg | Val | Ile | Asn | Tyr |
| Arg | Leu | Gln | Asn | Trp | Gly | Val | Ser | Arg | Gln | Arg | Tyr | Trp | Gly | Ala | Pro |
| Ile | Pro | Met | Ile | His | Cys | Lys | His | Cys | Gly | Ile | Val | Pro | Glu | Thr | Gln |
| Leu | Pro | Val | Thr | Leu | Pro | Glu | Asp | Ile | Val | Ile | Asp | Gly | Glu | Gly | Asn |
| Pro | Leu | Lys | Lys | His | Ala | Ser | Trp | Arg | Phe | Ala | Gln | Cys | Pro | Arg | Cys |
| His | Lys | Asp | Ala | Leu | Val | Glu | Thr | Asp | Thr | Met | Asp | Thr | Phe | Ile | Gln |
| Ser | Ser | Trp | Tyr | Phe | Leu | Arg | Tyr | Thr | Thr | Pro | Lys | Asn | Gln | Arg | Glu |
| Asn | Gln | Ala | Phe | Asp | Gln | Asn | Tyr | Leu | Lys | Tyr | Phe | Met | Pro | Val | Asp |
| Thr | Tyr | Ile | Gly | Gly | Ile | Glu | His | Ala | Ile | Leu | His | Leu | Leu | Tyr | Ala |
| Arg | Phe | Phe | Thr | Lys | Ala | Leu | Arg | Asp | Leu | Gly | Tyr | Leu | His | Leu | Asp |
| Glu | Pro | Phe | Lys | Gln | Leu | Ile | Thr | Gln | Gly | Met | Val | Leu | Lys | Asp | Gly |
| Ala | Lys | Met | Ser | Lys | Ser | Lys | Gly | Asn | Val | Val | Ser | Pro | Lys | Glu | Ile |
| Leu | Lys | Lys | Tyr | Gly | Ala | Asp | Ala | Val | Arg | Leu | Phe | Ile | Leu | Phe | Ala |
| Ala | Pro | Pro | Ala | Lys | Glu | Leu | Glu | Trp | Asn | Asp | Asn | Ala | Leu | Glu | Gly |

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Ala His Arg Phe Ile Lys Arg Leu Tyr Asp Lys Ala Asn Ala Ile Thr
 275 280 285
 Pro Thr Thr Ser Lys Pro Glu Phe Lys Glu Val Gly Leu Asn Glu Ala
 290 295 300
 Gln Lys Leu Ala Arg Lys Lys Val Tyr Glu Ala Leu Lys Lys Ser His
 305 310 315 320
 Glu Ile Phe Asn Lys Ala Glu Ser Ala Tyr Ala Phe Asn Thr Leu Ile
 325 330 335
 Ala Ser Cys Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu
 340 345 350
 Gln Ile Leu Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro
 355 360 365
 Met Ile Pro His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg
 370 375 380
 Glu Asn Phe Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp
 385 390 395 400
 Phe Met Thr Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu
 405 410 415
 Lys Val Asn Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys
 420 425 430
 Lys Glu Leu Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile
 435 440 445
 Tyr Val Pro Asn Lys Leu Val Asn Phe Val Thr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679

Leu Asn Leu Trp Leu Lys Ser Leu Met Arg Gly Asn Ser Ile Met Lys
 1 5 10 15
 Asn Ser His Gly Leu Lys Ala Phe Leu Glu Thr Lys Pro Lys Glu Tyr
 20 25 30
 His Lys Phe Asp Pro Ser Arg Phe Ile Gln Ile Tyr Lys Asp Phe Lys
 35 40 45
 Asn Ala Phe Phe Glu Ile Gln Ala Lys Val Ile His Val Val Gly Thr
 50 55 60
 Asn Gly Lys Gly Ser Thr Gly Arg Phe Leu Thr Leu Leu Leu Ala Asp
 65 70 75 80
 Gln Gly Phe Lys Val Leu His Phe Thr Ser Pro His Val Phe Glu Phe
 85 90 95
 Arg Glu Arg Phe Tyr Leu Asn Gly Ser Val Val Lys Glu Ser Val Leu
 100 105 110
 Glu Asn Ala His Gln Gln Leu Gln Ser His Ala Phe Ser Asn Ala Cys
 115 120 125
 Ser Tyr Phe Glu Tyr Ala Thr Leu Leu Ala Val Met Leu Ala Lys Asp
 130 135 140
 Cys Asp Tyr Leu Val Leu Glu Ala Gly Leu Gly Glu Phe Asp Ser

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```

145      150      155      160
Thr Asn Ala Leu Glu Lys Thr Leu Ser Val Phe Thr Pro Ile Asp Tyr
      165      170      175
Asp His Lys Glu Phe Leu Gly Asp Ser Leu Glu Ser Ile Ala Thr Thr
      180      185      190
Lys Leu Lys Ala Met Gly Ser Leu Asn Ile Ile Ala Pro Gln Gln Glu
      195      200      205
Leu Val Leu Asn Val Ala Gln Lys Ile Ala Lys Asp Lys His Ala Gln
      210      215      220
Leu Ile Val Val Gln Asn Glu Ile Ser Lys Gly Val Ser Asp Tyr Ile
      225      230      235
Glu Arg His His Leu Ala His Phe Leu Ala Met Asn Leu Glu Val Ala
      245      250      255
Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys Asn Lys Gln Glu Val Leu
      260      265      270
Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly Arg Cys Glu Leu Leu Ser
      275      280      285
Pro Asn Ile Leu Ile Asp Val Gly His Asn Pro His Ser Ala Lys Ala
      290      295      300
Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn Ala Pro Ile Val Leu Ile
      305      310      315
Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe Leu Val Leu Glu Ile Leu
      325      330      335
Lys Ser Val Val Lys Lys Val Leu Ile Leu Glu Leu His Asn Glu Arg
      340      345      350
Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile Leu Glu Thr Leu Gly Leu
      355      360      365
Glu His Ala Leu Phe Glu Glu Leu Lys Glu Asn Glu Asn Tyr Leu Val
      370      375      380
Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe Tyr Glu Arg Tyr Pro Lys
      385      390      395      400
Lys Arg Asp

```

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680

```

Ser Val Ser Ser His Ser Gly Ser Ala Asp Leu Leu Glu Asn Leu Gly
1      5      10      15
Val Asn Ile Glu Met Asn Pro Met Gln Leu Glu Asn Cys Phe Lys Gln
      20      25      30
Ser His Phe Gly Phe Leu Phe Ala Pro Leu Tyr His Gln Ser Phe Lys
      35      40      45
Lys Ser Ala Pro Leu Arg Lys Glu Leu Phe Thr Lys Thr Ile Phe Asn
      50      55      60
Cys Leu Gly Pro Leu Ile Asn Pro Leu Arg Pro Lys Ile Gln Leu Leu
      65      70      75      80

```

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Gly Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys
 85 90 95
 Ala Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Asp
 100 105 110
 Glu Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn
 115 120 125
 Glu Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro
 130 135 140
 Tyr Asp Leu Lys Glu Leu Gln Ile Glu Asn Ala Lys Glu Ser Val Gln
 145 150 155 160
 Ala Cys Leu Asp Ile Leu Glu Asn Lys Gly Lys Asp Ser His Thr Met
 165 170 175
 Val Val Ala Ala Asn Val Ala Ser Leu Leu Tyr Leu Ser His Arg Ala
 180 185 190
 Lys Gly Phe Lys Arg Gly Arg Glu His Asp Phe Arg Ala Phe Lys Asn
 195 200 205
 Gln Ser Ala Leu Cys Ala Phe Thr Lys Asn His Lys Ala Lys Pro Cys
 210 215 220
 Leu Ala Cys
 225

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681

Asn Leu Val Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly
 1 5 10 15
 Phe Asp Cys Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Ile
 20 25 30
 Glu Pro Ser Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Gly
 35 40 45
 Ile Pro Lys Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu
 50 55 60
 Ile Leu Lys Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His
 65 70 75 80
 Asn Lys Val Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile
 85 90 95
 Val Gly Ala Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp
 100 105 110
 Arg Glu Asn Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp
 115 120 125
 Asn Ile Thr Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu
 130 135 140
 Lys Lys Lys Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys
 145 150 155 160
 Ala Val Met Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg
 165 170 175
 His Leu Leu Pro Lys Arg Tyr Ser Val Gln Glu Ser Val Phe Asn Leu

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```

          180          185          190
Ser His Ala Ser Leu Met Thr Met Ala Ile Val Gln Gly Lys Trp Asp
          195          200          205
Leu Leu Arg Cys Cys Ser Lys Asp Arg Met His Gln Tyr Lys Arg Met
          210          215          220
Gln Thr Tyr Pro Val Leu Phe Ala Ile Gln Lys Leu Ala Leu Glu Asn
          225          230          235          240
Asn Ala Leu Met Ser Thr Leu Ser Gly Ser Gly Ser Ser Phe Phe Asn
          245          250          255
Met Cys Tyr Glu Glu Asp Ala Pro Lys Leu Lys Gln Val Leu Ser Lys
          260          265          270
Lys Phe Pro Lys Phe Arg Val Ala Val Leu Asp Phe Asp Asn Asp Gly
          275          280          285
Val Leu Ile Glu Lys Asp
          290

```

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682

```

Leu Val Phe Lys Lys Pro Phe Phe Lys Asn Arg Leu Leu Asn Val Thr
1          5          10          15
Asn Lys Leu Lys Phe Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn
          20          25          30
His Tyr Cys Arg Lys Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys
          35          40          45
Lys Gln Gly Ala Lys Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala
          50          55          60
Ala Met Ala Ile Ile Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val
          65          70          75          80
Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn
          85          90          95
Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val
          100          105          110
Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr
          115          120          125
Thr His Ile Ser Gly Ile Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr
          130          135          140
Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys
          145          150          155          160
Lys Tyr Gly Lys Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn
          165          170          175
Ser Lys Lys Gly Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys
          180          185          190
Ile Ser Leu Asp Val Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile
          195          200          205
Asn Ser Arg Trp Ser Pro Leu Ser Gly Gly Leu Asn Gly His Lys Tyr
          210          215          220

```

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Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe
 225 230 235 240
 Val Met Leu Ala Lys Glu Val Pro Asn Ala His Lys Arg Met Gly Asp
 245 250 255
 Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu
 260 265 270
 Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu
 275 280 285
 Ile Gln Asp His Glu Cys Ala Ile Leu Arg
 290 295

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683

Tyr His Arg Thr Asn Thr Thr Ile Arg Ile Ile Ile Met Gln Asp Leu
 1 5 10 15
 Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr His Asp Gly Thr
 20 25 30
 Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn Gly Asn Glu Ile
 35 40 45
 Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn Asn Leu Leu Gln
 50 55 60
 Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys Val Lys Gly Ser
 65 70 75 80
 Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn Ile Lys Leu Val
 85 90 95
 Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly Gln Ser Leu Ser
 100 105 110
 Leu Lys Ser Glu Phe Leu Lys Lys Ala
 115 120

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684

```

Lys Gly Cys Phe Met Arg Glu Phe Phe Lys Lys Leu Gly Thr Glu Tyr
1      5      10      15
Ala Ser Lys Leu Phe Leu Val Tyr Trp Leu Arg Trp Met Leu Ser Ala
      20      25      30
Leu Val Met Leu Pro Phe Met Glu Val Phe Tyr Tyr Phe Asn Phe Pro
      35      40      45
Leu Trp Leu Asn Leu Phe Leu Gly Gln Thr Ile Gly Ala Val Ile Phe
50      55      60
Phe Lys Leu Asp Lys Leu Ile Phe Ser Lys Lys
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 497 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685

```

Phe Phe Lys Arg Tyr Glu Arg Leu Ser Met Gln Tyr Ser Ser Leu Leu
1      5      10      15
Ser Val Val Leu Phe Leu Pro Leu Ile Gly Ala Val Tyr Ala Gly Leu
      20      25      30
Phe Gly Ala Lys Ala Lys Ala Leu His Val Gly Val Phe Asn Ser Leu
      35      40      45
Cys Val Leu Val Ser Phe Ile Gly Ala Val Val Leu Phe Ile Gln Ala
50      55      60
Trp His His Gln Ser Tyr Glu Lys Tyr Leu Phe Asp Trp Ile Val Val
65      70      75      80
Gly Asn Phe Lys Val Gly Phe Ser Leu Met Leu Asp Asn Ile Asn Ala
      85      90      95
Val Met Ile Val Val Val Thr Leu Val Ser Phe Leu Val His Val Tyr
      100      105      110
Ser Ile Gly Tyr Met Glu His Asp Thr Gly Phe Asn Arg Tyr Phe Ser
      115      120      125
Tyr Leu Ser Gly Phe Val Phe Ser Met Leu Val Leu Val Leu Ser Asp
      130      135      140
Asn Phe Leu Gly Leu Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser
145      150      155      160
Tyr Leu Leu Ile Gly Phe Trp Tyr His Lys Ser Ala Asn Asn Ala
      165      170      175
Ser Ile Glu Ala Phe Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu
      180      185      190
Met Gly Ile Ile Leu Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys
      195      200      205
Glu Val Phe Ser Met Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr
210      215      220

```

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```

Ile Ser Val Phe Leu Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe
225                230                235                240
Pro Met His Thr Trp Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val
                245                250                255
Ser Ala Leu Ile His Ala Ala Thr Met Val Thr Ala Gly Val Tyr Leu
                260                265                270
Ile Ile Arg Ala Asn Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr
                275                280                285
Phe Ile Ala Cys Leu Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met
                290                295                300
Ala Leu Val Asn Lys Asp Leu Lys Arg Ile Val Ala Tyr Ser Thr Leu
305                310                315                320
Ser Gln Leu Gly Tyr Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala
                325                330                335
Ile Ala Leu Phe His Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu
                340                345                350
Phe Leu Gly Ser Gly Asn Val Met His Ala Met Glu Asp Asn Leu Asp
355                360                365
Ile Thr Lys Met Gly Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val
370                375                380
Phe Met Ile Ile Gly Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala
385                390                395                400
Gly Tyr Phe Ser Lys Asp Lys Ile Leu Glu Val Ala Phe Gly Met His
                405                410                415
His His Ile Leu Trp Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala
                420                425                430
Phe Tyr Ser Phe Arg Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln
435                440                445
His Glu Ile Asn His Pro His Glu Gly Gln Lys Phe His Ala Phe Glu
450                455                460
His Ala Thr Val Arg Gly Phe Gly Gly His Cys Arg Phe Phe Arg Arg
465                470                475                480
Ala Val Phe Ser Phe Tyr Leu Ser Ser Glu Phe Leu Val Leu Glu Ser
                485                490                495
Ile

```

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686

```

Asn Lys Pro Asn Lys Gly Ala Val Leu Glu Lys Thr Lys Lys Arg Gln
1          5          10          15
Leu Leu Gln Lys Lys Thr Lys Lys Arg Ile Lys Gln Lys Arg Leu Pro
20          25          30
Gln Lys Lys Ile Lys Gln Lys Thr Arg Gln Arg Leu Lys Arg Lys Ile
35          40          45
Glu Val Pro Thr Lys Thr Thr Tyr Leu Leu Leu Glu Glu Ala Gly Ile

```

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```

      50              55              60
Asn Leu Glu Thr Tyr Glu Lys Ile Leu Ala Leu Leu Gln Lys Ser Asn
65              70              75              80
Asn Thr Leu Leu Val Val Gly Glu Glu Ile Tyr Ser His Lys Gln Ala
      85              90              95
His Asn Ile Ala Lys Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile
      100             105             110
Lys Leu Ile Leu Ile Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser
      115             120             125
Ile Cys Glu Leu Ser Glu Glu Val Phe Glu His Glu Lys Ile Val Gly
      130             135             140
Ile Arg Ala Gln Gly Asp Phe Thr Ile Asn Ser Asp Asp Arg Val Phe
145             150             155             160
Gly Lys Asp Ala Val Ser Lys Val Asp Phe Ile Leu Pro Ser Leu Asn
      165             170             175
Gln Leu Glu Gly Thr Ile Thr Asn Val Glu Gly Arg Val Leu Pro Leu
      180             185             190
Lys Pro Ala Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln
      195             200             205
Gly Phe Gly Phe Val Glu Glu Asn Leu Thr Glu Cys Thr His Lys Leu
      210             215             220
Pro Thr Glu Ala Gly Phe Lys Ala Leu Glu Phe Asp His Leu Thr Asn
225             230             235             240
Tyr Phe Thr Asn Asp Arg Ala Asn His Arg Gly Tyr Leu Leu Gly Thr
      245             250             255
Ser His Phe Glu Asn Ser Ala Lys Glu Ser Lys Pro Gln Asn Ala Ser
      260             265             270
Leu Ser Ser Leu
      275

```

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687

```

Gly Gly Phe Met Ala Lys Gln Glu Tyr Lys Gln Leu Pro Lys Arg Ala
1              5              10              15
Glu Val His Ser Ala Thr Glu Gln Phe Lys Asp Thr Ile Lys Thr Ser
      20              25              30
Leu Gly Leu Asp Leu Phe Lys Gly Leu Gly Leu Thr Ile Lys Glu Phe
      35              40              45
Phe Ser Pro Ser Val Thr Ile His Tyr Pro Met Glu Gln Leu Pro Leu
      50              55              60
Ser Pro Arg Tyr Arg Ala Val His His Leu Gln Arg Leu Leu Asp Ser
65              70              75              80
Gly Ser Glu Arg Cys Ile Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr
      85              90              95
Ser Asn Cys Ile Arg Ile Ile Thr His Lys Gly Glu Asp Asn Arg Lys
      100             105             110

```

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```

Lys Ile Asp Ser Tyr Thr Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly
    115          120          125
Leu Cys Ala Glu Val Cys Pro Glu Leu Ala Ile Val Met Gly Asn Arg
    130          135          140
Phe Glu Asn Ala Ser Thr Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu
    145          150          155          160
Phe Leu Thr Ser Glu Gln Asp Ala Lys Asn Cys Ser His Ala Glu Phe
    165          170          175
Leu Gly Phe Gly Ala Val Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala
    180          185          190
Thr Pro Leu Asp Tyr Val Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu
    195          200          205
Glu Ser Pro Thr Ser Pro Glu Ser His Lys Gly Asp Glu Asn Val
    210          215          220

```

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688

```

Ile Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Leu Gln
1          5          10          15
Gln Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala
    20          25          30
Phe Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile
    35          40          45
Thr Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met
    50          55          60
Val Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly
    65          70          75          80
Val Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala
    85          90          95
Phe Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys
    100          105          110
Gln Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu
    115          120          125
Leu Thr Leu Ile Leu Ser Ala Pro Ser Ile Gly Glu Asn Leu Ser Lys
    130          135          140
Gln Val Asn Ser Asn Ala Ile Asp Ala Gln Ile Pro Asn Ile Lys Ala
    145          150          155          160
Ile Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala
    165          170          175
Ala Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile
    180          185          190
Gln Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu
    195          200          205

```

(2) INFORMATION FOR SEQ ID NO:1689:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689

```

Met Lys Gln Phe Lys Lys Lys Pro Lys Lys Ile Lys Arg Ser His Gln
1      5      10      15
Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
20      25      30
Ile Gly Gly Phe Ala Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu
35      40      45
Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
50      55      60
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Lys Thr Gln Gln
65      70      75      80
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
85      90      95
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
100      105      110
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
115      120      125
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
130      135      140
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
145      150      155      160
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
165      170      175
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
180      185      190
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
195      200      205
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
210      215      220
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
225      230      235      240
Tyr Leu Gln Phe Phe Ser
245

```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690

```

Val Phe Thr Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Phe Leu Phe
1      5      10      15
Leu Ile Leu His Glu Ile Leu Asn Thr Glu Leu Ala Pro Leu Asn Gly
20      25      30
Ile Ser Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Leu Val Leu Ser
35      40      45
Ala Ser Leu Ile Phe Glu Lys Val Leu Ser Lys Gln Tyr Leu Gln Thr
50      55      60
Ala Lys Asp Lys Ile Ala Ser Leu Lys Asn Leu Lys Val Ile Ala Ile
65      70      75      80
Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu His Gln Ile
85      90      95
Leu Gln Thr Gln Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr
100     105     110
Leu Leu Gly Ile Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser
115     120     125
Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys
130     135     140
Glu Ile Thr Arg Leu Ile Glu Pro His Leu Ala Val Val Ala Glu Val
145     150     155     160
Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu
165     170     175
Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys
180     185     190
Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu
195     200     205
Ile Asp Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly
210     215     220
Thr Ser Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr
225     230     235     240
Lys Val Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu
245     250     255
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val
260     265     270
Phe Glu Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn
275     280     285
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met
290     295     300
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Gln Gly Arg Lys Val Ile
305     310     315     320
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu
325     330     335
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu
340     345     350
Leu Asn Ser Lys Thr Ile Ala Ser Lys Leu Lys Thr Pro Gln Lys Ile
355     360     365
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr
370     375     380
Ile Gln Gly Asp Leu Ile Leu Phe Ala Thr Asp Ala Pro Asn Tyr Ile
385     390     395     400

```

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691

```

Tyr Ala Leu Lys Ser Leu Arg Gln Ala Tyr Phe Phe Ser Gln Ser Val
1      5      10      15
Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe Glu
20     25     30
Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr Ile
35     40     45
Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala Arg
50     55     60
Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys Glu
65     70     75     80
Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn Gly
85     90     95
Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys Tyr
100    105    110
Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Gly Lys
115    120    125
Thr Ala Cys Val Ala Leu Pro Asn Leu Leu Thr Leu Pro Asn Ser Cys
130    135    140
Ile Ile Thr Asp Ile Lys Gly Glu Leu Arg Asp Lys Thr Ala Gly Tyr
145    150    155    160
Arg Gln Lys Phe Leu Asn Asn Arg Ile Leu Ile Phe Asn Pro Tyr Gly
165    170    175
Asp Asp Asn Thr Cys Tyr Phe Asn Pro Phe Asp Lys Arg Ile Val Glu
180    185    190
Lys Met Thr Phe Ala Glu Gln Leu Arg His Val Lys Ala Val Gly Asp
195    200    205
Gly Ile Phe Val Asp Glu Glu Asp His Trp Val Ser Lys Ala Lys Glu
210    215    220
Leu Phe Val Phe Phe Ala Leu Leu Gln Val Val Thr Lys Gly His Ser
225    230    235    240
Ser Phe Tyr Asp Val Ser Ile Ala Pro Ala Asn Asp Tyr Ala Pro Leu
245    250    255
Ile His Pro Lys Ser Pro Tyr Tyr Lys Gln Leu Tyr Gln His Asp Lys
260    265    270
Lys Thr Gly Glu Val Ile Leu Asp Pro Gln Thr Asn Ala Pro Met Lys
275    280    285
Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val Ala Asp
290    295    300
Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro Arg Glu
305    310    315    320
Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile Ile Arg
325    330    335
Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe Gly Ser
340    345    350
Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp Pro Lys
355    360    365
Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu Leu Arg
370    375    380
Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp Ile Gly
385    390    395    400

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SUBSTITUTE SHEET (RULE 26)

1233

Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala Lys Asn
 405 410 415
 Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe Ile Ile
 420 425 430
 Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu Glu Met
 435 440 445
 Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile Thr Gln
 450 455 460
 Asp Tyr Ala Met Ile Arg Lys Tyr Tyr Ser Asp Asp Asp Leu Lys Ile
 465 470 475 480
 Leu Lys Gly Val Val His Tyr Asn Ile Val Phe Lys Met Asn Ser Ala
 485 490 495
 Glu Asp Ala Glu Ile Val Ser Lys Glu Val Gly Glu Phe Thr Arg Arg
 500 505 510
 Ser Lys Asn Tyr Ser Thr Glu Lys Gly Gln Leu Val Phe Gly Gly Ser
 515 520 525
 Ser Ser Tyr Ser His Glu Gly Arg Asn Leu Leu Thr Ala Gln Asp Ile
 530 535 540
 Met Asn Ile Asn Ser Asp Glu Val Ile Val Ile Val Thr Gly Ala Lys
 545 550 555 560
 Ala Thr Pro Leu Lys Leu Lys Ala Asn Tyr Trp Phe Lys Asp Lys Glu
 565 570 575
 Leu Leu Lys Arg Ala Asn Leu Pro Ile Asp Leu Glu Val Glu Arg Gln
 580 585 590
 Arg Val Glu Glu Pro Ile Gln Pro Thr Thr Glu Ile Glu Thr Thr Pro
 595 600 605
 Asn Gln Asn Lys Ala Asp Leu Glu Pro Ser Asn Lys Gly Glu Lys Val
 610 615 620
 Glu Asn Glu Ser Asn Glu Arg Asn Thr Asn Glu Asn Asn Pro Thr Thr
 625 630 635 640
 Pro Gln Glu Leu Glu Asn Ser Asn Leu Lys Glu Ser Glu Lys Asp Asn
 645 650 655
 Glu Ser Pro Ile Thr Leu Glu Asn Ala Asn Glu Asn Ile Glu Gln Gly
 660 665 670
 Asn His Asn Glu Ile Asp Glu Ile Leu Lys Lys Pro Leu Ser Glu Ile
 675 680 685
 Ser Met Glu Glu Lys Arg Ala Leu Phe Lys Lys Met Gln Gln Ser Asp
 690 695 700
 Glu Glu Ser Glu Gln Glu Val Thr Gln Ser Thr Gln Ser
 705 710 715

(2) INFORMATION FOR SEQ ID NO:1692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2440 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692

Tyr Asn His Pro Asn Leu Ser Val Ala Asp Leu Glu Leu Glu Gln Gln
 1 5 10 15
 Asn Leu Gly Glu Gln Asn Gly Lys Glu Arg Thr Asn Arg Ala Asp Glu

SUBSTITUTE SHEET (RULE 26)

1234

| | | |
|---|-----|-----|
| 20 | 25 | 30 |
| Pro Asn Gly Thr Arg Ala Gly Ile Pro Gln Glu Ile His Arg Arg Ser | | |
| 35 | 40 | 45 |
| Glu Pro Arg Gly Gln Gln Glu Gly Met Glu Arg Ser Ser Asp Glu Asp | | |
| 50 | 55 | 60 |
| Leu Ser His Gln Asp Pro Ser Leu Phe Ile Glu Ser Arg Glu Gln Gly | | |
| 65 | 70 | 75 |
| Gly Thr Arg Gly Val Tyr Arg Ser Ser Asp Gln Gln Ala Val Ser Glu | | |
| 85 | 90 | 95 |
| Glu Ser His Arg Glu Arg Asp Arg Ile His Glu His Val Ser Arg Gly | | |
| 100 | 105 | 110 |
| Asp Gly Val Ser Ala Arg Ala Asp Ala Arg Ala Asn Ser Asn Gly Ala | | |
| 115 | 120 | 125 |
| Ser Ser Pro Ala Ser Arg Met Glu Asn Gly Ala Arg Ser Glu Glu Lys | | |
| 130 | 135 | 140 |
| Gly Asp Asn Pro Ser Asp Glu Arg Gly Ile Pro Gln Thr Pro Gln Ser | | |
| 145 | 150 | 155 |
| Pro Ser His Gln Gln Asn Ser Ser Arg Asp Leu Gly Leu Ser Leu Ser | | |
| 165 | 170 | 175 |
| Arg Glu Gln Pro Gly Gln Thr Gly Arg Leu Arg Leu Phe Asp His Gly | | |
| 180 | 185 | 190 |
| Gln Met Gly Ser Leu Phe Pro Thr Asp His Glu Asn Gln Arg Lys Arg | | |
| 195 | 200 | 205 |
| Ser Asp Asn Glu Leu Asp Arg Arg Ser Asp Lys Ala Asn Glu Asn Gly | | |
| 210 | 215 | 220 |
| Asp Lys Ser Pro Arg Gln Asn Gly Ser Ala Asn Gln Glu Ser Ala Arg | | |
| 225 | 230 | 235 |
| Ser Glu Arg Tyr Gly Ile Ala Gln Gly Ser Ser Asn Gln Ser Val Leu | | |
| 245 | 250 | 255 |
| Leu Pro Ala Gln Ser Arg Leu His His Ala Gly Leu Ser Ala Gln Asn | | |
| 260 | 265 | 270 |
| Gly Leu Arg Asp Leu Glu Glu Asn Arg Asp Gln Glu Gly Arg Leu Leu | | |
| 275 | 280 | 285 |
| Ser Asn Leu Asp Asn Leu Glu Ser Leu Leu Asn Ala Ile Arg Asn Asn | | |
| 290 | 295 | 300 |
| Thr Ile Ala Ser Glu Pro Asp Phe Arg Ser Arg Leu Leu Glu Ala Ile | | |
| 305 | 310 | 315 |
| Gln Asn Asn Asp Pro Leu Lys Asp Ser Ile Val Gly Ala Gln Leu Leu | | |
| 325 | 330 | 335 |
| Lys Asp Pro Thr Thr Lys Ile Phe Tyr Asp Lys Phe Gln Leu Lys Ile | | |
| 340 | 345 | 350 |
| Ser Pro Lys Lys Val Leu Glu Ile Leu Glu Asn Arg Leu Lys Lys Ser | | |
| 355 | 360 | 365 |
| Ile Glu Thr Thr Asn Glu Thr Leu Asn Ala Phe Asn Val Leu Asp Ser | | |
| 370 | 375 | 380 |
| Gln Ala Ile Asp Leu Asn Ala Ile Ser Asn Ser Val Gly Leu Asn Pro | | |
| 385 | 390 | 395 |
| Thr Gln Glu Ser Lys Ile Thr Asp Asn Ser Val Glu Leu Asn Asn Ala | | |
| 405 | 410 | 415 |
| Gln Glu Gln Thr Ala Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln | | |
| 420 | 425 | 430 |
| Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu | | |
| 435 | 440 | 445 |
| Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Asp Thr Gln Glu Asn | | |
| 450 | 455 | 460 |
| Ala Pro Thr Thr Ile Lys Gln Glu Thr Pro Ile Thr Pro Ala Ile Pro | | |
| 465 | 470 | 475 |
| Leu Asn Pro Lys Ile Asp Phe Lys Pro Ser Glu Glu Val Leu Ile Lys | | |
| 485 | 490 | 495 |
| Gly Ala Lys Thr Arg Tyr Lys Ala Asn Ile Lys Ala Ile Glu Leu Leu | | |
| 500 | 505 | 510 |
| Lys Glu Leu Gln Ala Lys Gln Glu Ile Leu Lys Gly Asp Tyr Tyr Ala | | |
| 515 | 520 | 525 |
| Thr Leu Lys Glu Gln Glu Ile Leu Ala Gln Phe Ser Gly Trp Gly Gly | | |
| 530 | 535 | 540 |

SUBSTITUTE SHEET (RULE 26)

1235

Leu Glu Ser Tyr Phe Lys Lys Ala Gln His Pro Glu Glu Phe Lys Glu
 545 550 555 560
 Leu Asn Ala Leu Leu Thr Lys Asp Glu Phe Arg Arg Ala Tyr Leu Ser
 565 570 575
 Ala Arg Asp Ala Tyr Tyr Thr Pro Lys Leu Val Ile Asp Ser Ile Tyr
 580 585 590
 Gln Gly Leu Asp Gln Leu Gly Phe Asn Asn Asp Asn His Pro Lys Lys
 595 600 605
 Ile Phe Glu Pro Ser Leu Gly Thr Gly Lys Phe Ile Ala His Ala Pro
 610 615 620
 Ser Asp Lys Asn Tyr Arg Phe Ile Gly Thr Glu Leu Asp Pro Ile Ser
 625 630 635 640
 Ala Asn Leu Ser Lys Phe Leu Tyr Pro Asn Gln Val Ile Gln Asn Thr
 645 650 655
 Ala Leu Glu Asn Tyr Gln Phe Tyr Gln Glu Tyr Asp Ala Phe Val Gly
 660 665 670
 Asn Pro Pro Tyr Gly Asn His Lys Ile Tyr Ser Ser Asn Asp Lys Glu
 675 680 685
 Leu Ser Asn Glu Ser Ile His Asn Tyr Phe Leu Gly Lys Ala Ile Lys
 690 695 700
 Glu Leu Lys Asp Asp Gly Ile Gly Ala Phe Val Val Ser Ser Trp Phe
 705 710 715 720
 Met Asp Ala Lys Asn Pro Lys Met Arg Glu His Ile Ala Lys Asn Ala
 725 730 735
 Thr Phe Leu Gly Ala Ile Arg Leu Pro Asn Ser Val Phe Lys Ala Thr
 740 745 750
 Gly Ala Glu Val Thr Ser Asp Ile Val Phe Phe Lys Lys Gly Val Glu
 755 760 765
 Lys Ala Thr Asn Gln Ser Phe Thr Lys Ala Met Pro Tyr Tyr Asp Lys
 770 775 780
 Ile Leu Asn Ser Leu Asp Asp Thr Leu Phe Ala Leu Gln Asn Asn
 785 790 795 800
 Arg Phe Asp Ser Phe Ile Pro Ser Asp Gln Leu Lys Ile Val Asn Ala
 805 810 815
 Val Ala Asn His Phe Gly Phe Lys Gln Glu Lys Leu Gln Arg Trp Tyr
 820 825 830
 Glu Lys Ile Asp Thr Ala Asn Phe Gly Tyr Ser Thr Gln Asp Tyr Lys
 835 840 845
 Ile Ile Lys Asp Phe Ile Asp Lys Val Gly Lys Asn Ser Ile Asn Leu
 850 855 860
 Asn Glu Gln Thr Leu Asn Glu Tyr Phe Ile His His Pro Glu Asn Ile
 865 870 875 880
 Leu Gly His Leu Ser Leu Glu Lys Thr Arg Tyr Arg Phe Glu Thr Asn
 885 890 895
 Gly Glu Gln Ile Tyr Lys Tyr Asp Leu Gln Ala Leu Glu Asp Glu Ser
 900 905 910
 Leu Asp Leu Ser Gln Ala Leu Lys Gln Ala Ile Glu Lys Leu Pro Lys
 915 920 925
 Asp Val Tyr Gln Tyr His Lys Thr Thr Leu Lys Thr Asp Val Leu Ile
 930 935 940
 Ile Asp Ser Ser Asn Glu Arg Tyr Gln Glu Val Gln Lys Leu Ile Lys
 945 950 955 960
 Asn Leu Glu Arg Arg Glu Leu Val Lys Trp Asp Asn Leu Tyr Phe Gln
 965 970 975
 Leu Glu Gln Asn Asn Glu Met Gly Ile Phe Leu Lys Pro Thr Lys Ile
 980 985 990
 Asn Ser Lys Val Gln Asp Ser Arg Leu Lys Ala Tyr Phe Lys Ile Lys
 995 1000 1005
 Asp Ala Leu Asn Asp Leu Thr Ser Ala Glu Leu Asn Pro Leu Ser Ser
 1010 1015 1020
 Asp Leu Glu Leu Glu Asn Lys Arg Ala Lys Leu Asn Leu Val Tyr Asp
 1025 1030 1035 1040
 Glu Phe Val Lys Lys Phe Gly Tyr Leu Asn Glu Asn Lys Asn Arg Lys
 1045 1050 1055
 Asp Ile Arg Gln Asp Leu Tyr Gly Ala Lys Val Leu Gly Leu Glu Lys

SUBSTITUTE SHEET (RULE 26)

1236

| | | |
|-----------------------------|---------------------|---------------------|
| 1060 | 1065 | 1070 |
| Asp Phe Glu Lys Glu Ile Thr | Pro Arg Ser Ala Lys | Met Gln Asn Ile |
| 1075 | 1080 | 1085 |
| Glu Pro Arg Gln Ala Gln Ala | Lys Lys Ala Gln Ile | Phe Phe Glu Arg |
| 1090 | 1095 | 1100 |
| Thr Leu Asn Pro Lys Lys Glu | Leu Ile Ile Thr | Asn Ala Lys Glu Ala |
| 1105 | 1110 | 1115 |
| Leu Ile Ala Ser Ile Asn Gln | Lys Gly Gly Leu Asp | Leu His Phe Ile |
| 1125 | 1130 | 1135 |
| Arg Asp His Phe Thr Thr Gln | Ser Leu Glu Thr Thr | Ile Lys Glu Leu |
| 1140 | 1145 | 1150 |
| Leu Glu Gln Lys Leu Ile Tyr | Lys Asp His Lys Asp | Asn Gly Gly Tyr |
| 1155 | 1160 | 1165 |
| Ile Leu Ala Asn Asp Tyr Leu | Ser Gly Asn Val Lys | Arg Lys Leu Lys |
| 1170 | 1175 | 1180 |
| Glu Val Lys Glu Ala Ile Asn | Gln Gly Val Glu Gly | Leu Glu Ala Asn |
| 1185 | 1190 | 1195 |
| Val Lys Asp Leu Glu Leu Ile | Ile Pro Lys Asp | Leu Lys Ala Thr Glu |
| 1205 | 1210 | 1215 |
| Ile Met Ala Asn Ile Asn Ser | Pro Trp Ile Pro Thr | Gln Tyr Leu Glu |
| 1220 | 1225 | 1230 |
| Glu Phe Leu Met Glu Leu Ser | Ala Asn His Tyr Glu | Lys Gln Tyr Gly |
| 1235 | 1240 | 1245 |
| Asp Lys Met Thr Asp Tyr Gln | Leu Ser Asn Leu Lys | Glu Asp Ile Lys |
| 1250 | 1255 | 1260 |
| Ile Glu His Leu Ser Gly Ala | Tyr Glu Val Phe Val | Arg Asn Asn Glu |
| 1265 | 1270 | 1275 |
| Leu Asn Glu Leu Tyr Gly Ile | Arg His Lys Asp | Lys Pro His Ser Tyr |
| 1285 | 1290 | 1295 |
| Lys Val Pro Phe Glu Ser Leu | Leu Asn Lys Val Leu | Asn Asn Lys Asp |
| 1300 | 1305 | 1310 |
| Leu Ser Val Lys Tyr Ala Gln | Val Asp Pro Asn Asp | Pro Lys Lys Glu |
| 1315 | 1320 | 1325 |
| Ile Phe Ile Thr Asp Glu Glu | Gln Ser Asn Leu Ala | Arg Gln Lys Ala |
| 1330 | 1335 | 1340 |
| Glu Glu Leu Lys Glu Ala Phe | Lys Asp Trp Ile Tyr | Lys Asp Tyr Ser |
| 1345 | 1350 | 1355 |
| Arg Arg Thr His Leu Glu Gln | Ile Tyr Asn Asp | Thr Phe Asn Asn Phe |
| 1365 | 1370 | 1375 |
| Val Leu Lys Thr Tyr Asp Gly | Ser Gln Leu Glu Leu | Glu Gly Phe Asn |
| 1380 | 1385 | 1390 |
| Tyr His Ile Ser Leu Arg Pro | His Gln Lys Asn Ala | Ile Phe Arg Thr |
| 1395 | 1400 | 1405 |
| Ile Gln Asp Arg Ala Val Cys | Leu Asp His Gln Val | Gly Ala Gly Lys |
| 1410 | 1415 | 1420 |
| Thr Leu Cys Ala Ile Ala Ser | Cys Met Glu Gln Lys | Arg Met Gly Leu |
| 1425 | 1430 | 1435 |
| Val Asn Lys Thr Leu Ile Ala | Val Pro Asn His Leu | Thr Lys Gln Trp |
| 1445 | 1450 | 1455 |
| Gly Asp Glu Phe Tyr Lys Ala | Tyr Pro Asn Ala Asn | Val Leu Val Val |
| 1460 | 1465 | 1470 |
| Asp Ser Lys Asp Thr Thr Glu | Lys Arg Glu Leu Leu | Phe Asn Gln |
| 1475 | 1480 | 1485 |
| Ile Ala Asn Asn Asn Tyr Asp | Ala Val Val Ile Ala | His Thr His Leu |
| 1490 | 1495 | 1500 |
| Glu Leu Leu Ser Asn Pro Arg | Gly Ile Ile Glu Glu | Lys Lys Glu Glu |
| 1505 | 1510 | 1515 |
| Glu Leu Val Asn Ala Glu Lys | Asn Phe Glu Arg Gln | Glu Leu Ala Tyr |
| 1525 | 1530 | 1535 |
| Lys Asn Asn Pro Arg Glu Thr | Lys Lys Pro Asn Glu | Arg Ala Phe Lys |
| 1540 | 1545 | 1550 |
| Asn Lys Leu Asp Lys Ile Arg | Ala Lys Tyr Asp | Ala Ile Leu Glu Lys |
| 1555 | 1560 | 1565 |
| Gln Gly Ser His Ile Asp Ile | Ser Gln Met Gly Ile | Asp Asn Leu Ile |
| 1570 | 1575 | 1580 |

SUBSTITUTE SHEET (RULE 26)

1237

Val Asp Glu Ala His Leu Phe Lys Asn Leu Ala Phe Glu Thr Ser Met
1585 1590 1595 1600
Glu Lys Ile Ala Gly Leu Gly Asn Gln Gln Gly Ser Asn Arg Ala Arg
1605 1610 1615
Asp Leu Phe Ile Lys Thr Arg Tyr Leu His Gln Asn Asp Lys Lys Ile
1620 1625 1630
Met Phe Leu Thr Gly Thr Pro Ile Ala Asn Ser Leu Ser Glu Met Tyr
1635 1640 1645
His Leu Gln Arg Tyr Leu Thr Pro Asp Val Leu Lys Glu Arg Gly Leu
1650 1655 1660
Glu Phe Phe Asp Asp Trp Ala Lys Thr Tyr Gly Glu Val Val Asn Asp
1665 1670 1675 1680
Phe Glu Leu Asp Thr Ser Ala Gln Ser Tyr Lys Met Val Asn Arg Phe
1685 1690 1695
Ser Lys Phe Ser Asp Val Gln Gly Leu Ser Thr Met Tyr Arg Ala Phe
1700 1705 1710
Ala Asp Ile Val Ser Asn Asp Asp Ile Leu Lys His Asn Pro His Phe
1715 1720 1725
Val Pro Lys Val Tyr Gly Asp Lys Pro Ile Asn Val Val Lys Arg
1730 1735 1740
Ser Glu Glu Val Ala Gln Phe Ile Gly Val Ala Leu Glu Asn Gly Lys
1745 1750 1755 1760
Tyr Asn Glu Gly Ser Ile Ile Asp Arg Met Gln Lys Cys Glu Gly Lys
1765 1770 1775
Lys Ser Gln Lys Gly Gln Asp Asn Ile Leu Ser Cys Thr Thr Asp Ala
1780 1785 1790
Arg Lys Val Ala Leu Asp Tyr Arg Leu Ile Asp Pro Asn Ala Lys Val
1795 1800 1805
Glu Lys Glu Phe Ser Lys Ser Tyr Ala Met Ala Lys Asn Ile Tyr Glu
1810 1815 1820
Asn Tyr Leu Glu Thr His Ala Thr Lys Gly Thr Gln Leu Gly Phe Ile
1825 1830 1835 1840
Gly Leu Ser Thr Pro Lys Thr His Ser Gln Lys Val Ser Leu Glu Ala
1845 1850 1855
Leu Asp Asn Ala His Glu Thr Glu Asn Lys Asn Pro Leu Asp Lys Ala
1860 1865 1870
Gln Glu Leu Leu Glu Ser Leu Ser Ser Tyr Asp Glu Lys Gly Asn Leu
1875 1880 1885
Ile Ala Pro Ser Lys Lys Glu Leu Glu Asn Glu Leu Lys Glu Lys Glu
1890 1895 1900
Ala Lys Ser Val Asn Leu Asp Glu Glu Ile Ala Lys Gly Cys Ser Phe
1905 1910 1915 1920
Asp Val Tyr Ser Asp Val Leu Arg His Leu Val Gln Met Gly Ile Pro
1925 1930 1935
Gln Asn Glu Ile Ala Phe Ile His Asp Ala Lys Thr Glu Glu Gln Lys
1940 1945 1950
Gln Asp Leu Phe Lys Lys Leu Asn Arg Gly Gly Val Arg Val Leu Leu
1955 1960 1965
Gly Ser Pro Ala Lys Met Gly Val Gly Thr Asn Val Gln Glu Arg Leu
1970 1975 1980
Val Ala Met His Glu Leu Asp Cys Pro Trp Arg Pro Asp Glu Leu Leu
1985 1990 1995 2000
Gln Met Glu Gly Arg Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn
2005 2010 2015
Asp Pro Glu Asn Phe Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys
2020 2025 2030
Thr Tyr Asp Ser Arg Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly
2035 2040 2045
Ile Glu Gln Phe Arg Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu
2050 2055 2060
Asp Phe Asn Met Gly Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala
2065 2070 2075 2080
Thr Gly Asn Pro Leu Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile
2085 2090 2095
Lys Ser Glu Glu Ser Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe

SUBSTITUTE SHEET (RULE 26)

1238

| | | |
|---|---|------|
| 2100 | 2105 | 2110 |
| Asn Glu Glu Ser Leu Lys | Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys | |
| 2115 | 2120 | 2125 |
| Gln Glu Leu Lys Asp Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro | | |
| 2130 | 2135 | 2140 |
| Thr His Thr Glu Ile Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys | | |
| 2145 | 2150 | 2155 |
| Asp Tyr Glu Leu Ile Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn | | |
| 2165 | 2170 | 2175 |
| Ala Ser Met Ser Glu Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn | | |
| 2180 | 2185 | 2190 |
| Lys Gln Ile Ala Glu Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys | | |
| 2195 | 2200 | 2205 |
| Gln Phe Ala Ser Asn Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp | | |
| 2210 | 2215 | 2220 |
| Tyr Lys Leu Leu Glu Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr | | |
| 2225 | 2230 | 2235 |
| Lys Tyr Gln Val Glu Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile | | |
| 2245 | 2250 | 2255 |
| Ala Tyr Ser Pro Ser Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met | | |
| 2260 | 2265 | 2270 |
| Phe Ser Ser Tyr Asn Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu | | |
| 2275 | 2280 | 2285 |
| Lys Arg Leu Asp Asn Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu | | |
| 2290 | 2295 | 2300 |
| Leu Glu Asn Ser Ile Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr | | |
| 2305 | 2310 | 2315 |
| Arg Leu Val Glu Gln Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln | | |
| 2325 | 2330 | 2335 |
| Ala Leu Lys Trp Asp His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met | | |
| 2340 | 2345 | 2350 |
| Ser Lys Asp Arg Asn Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu | | |
| 2355 | 2360 | 2365 |
| Val Leu Lys Asn Leu Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu | | |
| 2370 | 2375 | 2380 |
| Arg Glu Glu Gln Gly Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile | | |
| 2385 | 2390 | 2395 |
| Glu Pro Ala Thr Glu Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp | | |
| 2405 | 2410 | 2415 |
| Glu Ile Ala Asn Asn Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu | | |
| 2420 | 2425 | 2430 |
| Ile Thr Lys Ser Met Gly Arg Arg | | |
| 2435 | 2440 | |

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693

SUBSTITUTE SHEET (RULE 26)

1239

```

Arg Glu Gly Ala Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val
1      5      10      15
Glu Pro Ser Gln Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser
20      25      30
Phe Phe His Ala Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe
35      40      45
Met Ile Trp Ala Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe
50      55      60
Lys Thr Ala Met Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile
65      70      75      80
Asn Trp Gly Ile Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn
85      90      95
Thr Ile Phe Tyr Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser
100     105     110
Leu Asn Asp Gly Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser
115     120     125
Glu Ile Phe Ser Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile
130     135     140
Val Asn Leu Trp Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp
145     150     155     160
Leu Thr Met Ile Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly
165     170     175
Glu Leu Leu Phe Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr
180     185     190
Ala Glu Ile Phe Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu
195     200     205
Gly Leu Ile Pro Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys
210     215     220
Leu Ile Ser Leu Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe
225     230     235     240
Phe Asn Tyr Gly Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys
245     250     255
His Glu Val Thr Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn
260     265     270
Glu Gly Lys Ile Ile Asp Val Phe Gly Asn Val Leu Lys Gly Asp Trp
275     280     285
Asn Ser Tyr Ile Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile
290     295     300
Val Leu Gly Ser Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp
305     310     315     320
Phe Ile Asn Asn Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr
325     330     335
Glu Met Met Gln Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly
340     345     350
Gly Ser Ala Val Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser
355     360     365
Ala Gly Gly Gly Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly
370     375     380
Leu Gly Ala Ile Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser
385     390     395     400
Val Lys Ala Gly Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe
405     410     415
Gly Phe Asp Asn Asp Lys Asn Asn Lys
420     425

```

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

1240

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694

```

Lys Glu Gln Gln Met Ala Tyr Lys Pro Asn Lys Lys Lys Leu Lys Glu
1      5      10      15
Leu Arg Glu Gln Pro Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val
20      25      30
Ala Thr Asn Asn Pro Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln
35      40      45
Glu Pro Leu Pro Tyr Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met
50      55      60
Ile Ser Arg Asp Pro Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys
65      70      75      80
Arg Val Tyr Lys Asp Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn
85      90      95
Gly Glu Ile Lys Glu Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly
100     105     110
Phe Glu Arg Arg Ile Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile
115     120     125
Asp Arg Asn Arg Glu Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His
130     135     140
Thr Asn Ser Leu Lys Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu
145     150     155     160
Thr His His Asn Glu Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu
165     170     175
Ile Val Lys Glu Tyr Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu
180     185     190
Arg Thr Lys Asp Gly Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser
195     200     205
Ser Ala Glu Tyr Phe Lys Leu Tyr Asn Lys Leu Pro Phe Glu Ser Ile
210     215     220
Asn Asn Glu Asn Thr Lys Leu Asn Thr Asn Asp Asn Glu Glu Val Lys
225     230     235     240
Lys Leu Glu Phe Glu Leu Ala Lys Glu Val His Ile Leu Ile Leu Glu
245     250     255
Gln Gln Leu Leu Ser Ala Thr Asn Tyr Tyr Ser Trp Ile Asp Lys Asp
260     265     270
Asp Asn Ala Asn Phe Ala Trp Lys Met His Arg Leu Ile Asn Glu Asn
275     280     285
Lys Leu Lys Glu Asn His Leu Ser Ala Asn Asn Ala Asn Lys Ile Lys
290     295     300
Gln Phe Phe Phe Asn Asn Gly Ser Ile Leu Gly Trp Thr Lys Glu Glu
305     310     315     320
Gln Ser Ala Ile Gln Glu Asn Arg Asp Tyr Ser Leu Arg Ser Ala Leu
325     330     335
Leu Ser Leu Glu Glu Ile Ala Gln Ala Lys Ile Glu Leu Gln Lys Tyr
340     345     350
Tyr Glu Ser Val Tyr Val Asn Gly Asp Gly Asn Lys Arg Glu Ile Lys
355     360     365
Pro Phe Lys Glu Ile Leu Arg Asp Thr Asn Asn Phe Glu Lys Ala Tyr
370     375     380
Lys Glu Arg Tyr Asp Lys Leu Val Ser Leu Ser Ala Ala Ile Ile Gln
385     390     395     400
Ala Lys Glu Gly Gly Asn Glu Arg Gln Asn Ser Ser Ala Asn Asn Asn
405     410     415
Asn Pro Ile Lys Asn Thr Ile Glu Thr Asn Thr Ser Asn Asn Ile Ile
420     425     430

```

SUBSTITUTE SHEET (RULE 26)

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Gln Asn Asn Asp Asn Ile Ile Ile Gln Ile
435 440

(2) INFORMATION FOR SEQ ID NO:1695:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695

Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe Arg His
1 5 10 15
Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val Leu Thr
20 25 30
Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile Tyr Ile
35 40 45
His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe Asp Ser
50 55 60
Leu Ile Glu Asn Lys Lys
65 70

(2) INFORMATION FOR SEQ ID NO:1696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696

Lys Lys Arg Lys Tyr Met Arg Phe Arg Arg Val Lys Lys His Lys Asn
1 5 10 15
Lys His Asn Lys Glu His Thr Ser Met Asp Leu Gln Gln Ile Asp Glu
20 25 30
Leu Glu Lys Lys Phe Glu Glu Gln Glu Gln Ala Gln Asp Thr Pro
35 40 45
Leu Lys Gln Glu Pro Ser Thr Lys Glu Val Lys Ile Pro Lys Lys Arg
50 55 60
Gly Arg Lys Lys Ser Leu Leu Asp Glu Asp Lys Lys Lys Ser Phe Asn

SUBSTITUTE SHEET (RULE 26)

1242

```

65      70      75      80
Ile Ala Phe Ser Pro Cys Val Ile Lys Glu Leu Asn Glu Phe Leu Leu
      85      90      95
Glu Phe Gly Ser Phe Lys Glu Thr Arg Ser Thr Phe Ile Glu Glu Ala
      100      105      110
Leu Ile Arg His Leu Lys His Arg Lys Asn Thr Gln Glu Gln Lys Leu
      115      120      125
Leu Lys Gln Leu Glu Arg Leu Gln Asn Lys Glu Lys Gly Asn Asn Glu
      130      135      140
Asn Asn Glu Leu Glu
145

```

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697

```

Leu Asn Thr Asp Lys Ile Thr Lys Tyr Leu Ile Ile Ile Asp Ile Phe
1      5      10      15
Leu Lys Leu Tyr Val Ile Met Ile Ser Glu Ile Ile Lys Phe Gln Leu
      20      25      30
Lys Gly Ile Lys Met Ile Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys
      35      40      45
Thr Ser Leu Leu Ala Gly Val Leu Leu Gly Ala Thr Ala Pro Leu Met
      50      55      60
Ala Lys Pro Leu Leu Ser Asp Glu Asp Leu Leu Lys Arg Val Lys Leu
      65      70      75      80
His Asn Ile Lys Glu Asp Thr Leu Thr Ser Cys Asn Ala Lys Val Asp
      85      90      95
Gly Ser Gln Tyr Leu Asn Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro
      100      105      110
Gln Glu Tyr Arg Glu Lys Ile Phe Glu Cys Val Glu Glu Glu Lys His
      115      120      125
Lys Gln Ala Leu Asn Leu Ile Asn Lys Glu Asp Thr Lys Asp Lys Glu
      130      135      140
Glu Leu Ala Lys Lys Ile Lys Glu Ile Lys Glu Lys Ala Lys Val Leu
      145      150      155      160
Arg Gln Lys Phe Met Ala Phe Glu Met Lys Glu His Ser Lys Glu Phe
      165      170      175
Pro Asn Lys Lys Gln Leu Gln Thr Met Leu Glu Asn Ala Phe Asp Asn
      180      185      190
Gly Ala Glu Ser Phe Ile Asp Asp Trp His Glu Arg Phe Gly Gly Ile
      195      200      205
Ser Arg Glu Asn Thr Tyr Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp
      210      215      220
Glu Gly Lys Ile Leu Ala Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr
      225      230      235      240
Lys Lys Asp Phe Glu Glu Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser
      245      250      255

```

SUBSTITUTE SHEET (RULE 26)

1243

Ala Met Ala Asn Met Ser Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu
 260 265 270
 Lys Pro Lys Tyr Gln Leu His Ser Ser Asn Asn Ile Lys Pro Leu Met
 275 280 285
 Ser Asn Thr Glu Leu Leu Asn Met Ile Glu Leu Thr Asn Ile Lys Lys
 290 295 300
 Glu Tyr Val Met Gly Cys Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro
 305 310 315 320
 Ile His Lys Asp Trp Gly Phe Phe Gly Lys Ala Lys Val Pro Glu Thr
 325 330 335
 Trp Arg Asn Lys Ile Trp Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr
 340 345 350
 Asp Asn Thr Thr Ala Glu Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr
 355 360 365
 Ser Ile Ser His His
 370

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698

Lys Asp Tyr Lys Thr Lys Lys Arg Ala Ile Met Lys Thr Met Asn Leu
 1 5 10 15
 Asn Glu Phe Phe Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys
 20 25 30
 Phe Lys Asp Thr Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu
 35 40 45
 Lys Leu Ile Leu Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile
 50 55 60
 Ser Asn Glu Asn Ala Pro Lys Ile Leu Ile Ser Arg Leu Met Cys Lys
 65 70 75 80
 Phe Ser Pro Ile Asp Tyr Glu Ser Thr Ile Pro Ser Asp Phe Lys Pro
 85 90 95
 Ile Asp Glu Glu Glu Tyr Glu Asp Asp Leu Glu Trp Leu Asn Glu Glu
 100 105 110
 Lys Glu Asp Arg Leu Phe Asn Tyr Tyr Leu Phe Leu Asn Gly Ile Lys
 115 120 125
 Glu Ser Asp Val Glu Glu Val Phe Asn Glu Ser Val Glu Ile Tyr Asp
 130 135 140
 Glu Cys Leu Ile Glu Ile Ala Gln Asn Val Leu Lys Asp Lys Phe Ser
 145 150 155 160
 Tyr Asp Ile Asp Leu Leu Gln Val Leu Val Lys Gly Tyr Ala Lys Glu
 165 170 175
 Ile Arg Glu Phe Leu Ser Tyr Lys Pro Ile Lys Glu Ile Lys Asp Phe
 180 185 190
 Lys Asp Lys Asp Thr Ala Leu Tyr Ile Ser Leu Gly Lys Asp Tyr Asp
 195 200 205
 Lys Glu Lys Glu Pro Phe Ser Lys Lys Leu Gln Gln Cys Phe Lys Glu

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210 215 220
 Ile Leu Glu Ser Lys Gly Ile
 225 230

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699

Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
 1 5 10 15
 Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
 20 25 30
 Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
 35 40 45
 Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
 50 55 60
 Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
 65 70 75 80
 Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
 85 90 95
 Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
 100 105 110
 Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
 115 120 125
 Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
 130 135 140
 Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
 145 150 155 160
 Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
 165 170 175
 Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
 180 185 190
 Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
 195 200 205
 Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
 210 215 220
 Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Val Asn Asp
 225 230 235 240
 Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
 245 250 255
 Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
 260 265 270
 Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
 275 280 285
 Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
 290 295 300
 Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Thr Lys Ala Ser Asn
 305 310 315 320

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1245

```

Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
      325      330      335
Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
      340      345      350
Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr
      355      360      365
Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
      370      375      380
Lys Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
      385      390      395      400
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
      405      410      415
Phe Ser Ile Trp Asp
      420

```

(2) INFORMATION FOR SEQ ID NO:1700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700

```

Lys Arg Trp Trp Tyr Phe Val Arg Ala Phe Leu Asn Arg Ser Phe Ala
1      5      10      15
Pro Leu Leu Asn Pro Asn Glu Asn Leu Leu Asp Gln Val Lys Ser Ser
      20      25      30
Ile Ile Leu Lys Lys Gly Val Ser Tyr Phe Asp Trp Gly Ala Ser Gly
      35      40      45
Leu Ala Ser Ala Leu Val Glu Lys Arg Val Lys Ser Leu Leu Pro Tyr
      50      55      60
Tyr Ala Asn Ala His Ser Val Ala Ser Lys His Ala Ile Leu Met Gly
      65      70      75      80
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
      85      90      95
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
      100      105      110
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
      115      120      125
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
      130      135      140
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
      145      150      155      160
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
      165      170      175
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
      180      185      190
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
      195      200      205
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
      210      215      220
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr

```

SUBSTITUTE SHEET (RULE 26)

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```

225          230          235          240
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
          245          250          255
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
          260          265          270
Pro Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
          275          280          285
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
          290          295          300
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
305          310          315          320
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
          325          330          335
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
          340          345          350
Asn Leu Thr Ala Ser Arg Val Gly Val Val Ala Phe Asn Ile Gly Gly
          355          360          365
Ile Ser Pro Tyr Asp Leu Ala Arg Val Leu Ser Tyr Glu Tyr Ala Ile
          370          375          380
Glu Thr Arg Ala Gly Cys Ser Cys Ala Gly Pro Tyr Gly His Asp Leu
385          390          395          400
Leu Asn Leu Asn Ala Gln Lys Ser Ser Asp Phe Asn Ala Lys Pro Gly
          405          410          415
Trp Leu Arg Val Ser Leu His Phe Thr His Ser Ile Asn Asp Ile Asp
          420          425          430
Tyr Leu Leu Asp Ser Leu Lys Lys Ala Val Lys Lys Leu Arg
          435          440          445

```

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature.
 (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701

```

Tyr Val Ile Glu Leu Asp Ile Asn Ala Ser Asp Lys Ser Leu Ser His
1          5          10          15
Arg Ala Val Ile Phe Ser Leu Leu Ala Gln Lys Pro Cys Phe Val Arg
          20          25          30
Asn Phe Leu Met Gly Glu Asp Cys Leu Ser Ser Leu Glu Ile Ala Gln
          35          40          45
Asn Leu Gly Ala Lys Val Glu Asn Thr Ala Lys Asn Ser Phe Lys Ile
          50          55          60
Thr Pro Pro Thr Thr Ile Lys Glu Pro Asn Lys Ile Leu Asn Cys Asn
65          70          75          80
Asn Ser Gly Thr Ser Met Arg Leu Tyr Ser Gly Leu Leu Ser Ala Gln
          85          90          95
Lys Gly Leu Phe Val Leu Ser Gly Asp Asn Ser Leu Asn Ala Arg Pro
          100          105          110
Met Lys Arg Ile Ile Glu Pro Leu Lys Ala Phe Gly Ala Lys Ile Leu
          115          120          125

```

SUBSTITUTE SHEET (RULE 26)

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Gly Arg Glu Asp Asn His Phe Ala Pro Leu Ala Ile Val Gly Gly Pro
 130 135 140
 Leu Lys Ala Cys Asp Tyr Glu Ser Pro Ile Ala Ser Ala Gln Val Lys
 145 150 155 160
 Ser Ala Phe Ile Leu Ser Ala Leu Gln Ala Gln Gly Ile Ser Ala Tyr
 165 170 175
 Lys Glu Ser Glu Leu Ser Arg Asn His Thr Glu Ile Met Leu Lys Ser
 180 185 190
 Leu Gly Ala Asn Ile Gln Asn Gln Asp Gly Val Leu Lys Ile Ser Pro
 195 200 205
 Leu Glu Lys Pro Leu Glu Ser Phe Asp Phe Thr Ile Ala Asn Asp Pro
 210 215 220
 Ser Ser Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr Pro Lys Ser
 225 230 235 240
 Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg Ile Glu Ala
 245 250 255
 Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr Val Ile Gln
 260 265 270
 Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu His Ala Pro
 275 280 285
 Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu Ile Asp Glu
 290 295 300
 Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly Lys Ser Met
 305 310 315 320
 Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp Arg Ile Lys
 325 330 335
 Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys Glu Glu Phe
 340 345 350
 Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser Gln Leu Lys
 355 360 365
 Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser Phe Asn Asp
 370 375 380
 His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala Leu Pro Leu
 385 390 395 400
 Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro Thr Phe Gln
 405 410 415
 Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly Asn
 420 425 430

(2) INFORMATION FOR SEQ ID NO:1702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702

Asn Ala Arg Thr Phe Leu Ser Gln Pro Phe Ser Phe Gly Ser Ile Tyr
 1 5 10 15
 Ser Lys Lys Gly Val Ser Met Glu Ile Lys Met Ala Lys Asp Tyr Gly
 20 25 30
 Phe Cys Phe Gly Val Lys Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln

SUBSTITUTE SHEET (RULE 26)

1248

```

      35              40              45
Asn Ser Leu Ile Phe Gly Ser Leu Ile His Asn Ala Lys Glu Ile Asn
 50              55              60
Arg Leu Glu Lys Asn Phe Asn Val Lys Ile Glu Glu Asp Pro Lys Lys
 65              70              75              80
Ile Pro Lys Asn Lys Ser Val Ile Ile Arg Thr His Gly Ile Pro Lys
      85              90              95
Gln Asp Leu Glu Tyr Leu Lys Asn Lys Gly Val Lys Ile Thr Asp Ala
      100              105              110
Thr Cys Pro Tyr Val Ile Lys Pro Gln Gln Ile Val Glu Ser Met Ser
      115              120              125
Lys Glu Gly Tyr Gln Ile Val Leu Phe Gly Asp Ile Asn His Pro Glu
      130              135              140
Val Lys Gly Val Ile Ser Tyr Ala Thr Asn Gln Ala Leu Val Val Asn
      145              150              155              160
Ser Leu Glu Glu Leu Gln Glu Lys Lys Leu Gln Arg Lys Val Ala Leu
      165              170              175
Val Ser Gln Thr Thr Lys Gln Thr Pro Lys Leu Leu Gln Ile Ala Ser
      180              185              190

```

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703

```

Lys Leu Pro Ile His Ala Phe Val Leu Met Cys Leu Ala Ile Pro Ser
1              5              10              15
Lys Val Ile Ala Ile Asn Asp Asn Val Ala Leu Leu Glu Thr Leu Gly
      20              25              30
Val Gln Arg Glu Ala Ser Leu Asp Leu Met Gly Glu Ser Val Lys Val
      35              40              45
Gly Asp Tyr Val Leu Leu His Ile Gly Tyr Val Met Ser Lys Ile Asp
      50              55              60
Glu Lys Glu Ala Leu Glu Ser Ile Glu Leu Tyr Gln Glu Met Ile Ala
      65              70              75              80
Glu Val Asn Glu Thr His Glu
      85

```

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704

```

Lys Gly Thr Ser Met Ser Glu Gln Arg Lys Glu Ser Leu Gln Asn Asn
1      5      10      15
Pro Asn Leu Ser Lys Lys Asp Ile Lys Ile Val Glu Lys Ile Leu Ser
20     25     30
Lys Asn Asp Ile Lys Ala Ala Glu Met Lys Glu Arg Tyr Leu Lys Glu
35     40     45
Gly Ser Val Cys Val Asn Phe Met Ser Ser Pro Gly Ser Gly Lys Thr
50     55     60
Thr Met Leu Glu Asn Leu Ala Asp Phe Lys Asp Phe Lys Phe Cys Val
65     70     75     80
Val Glu Gly Asp Leu Gln Thr Asn Arg Asp Ala Asp Arg Leu Arg Lys
85     90     95
Lys Gly Val Ser Ala His Gln Ile Thr Thr Gly Glu Ala Cys His Leu
100    105    110
Glu Ala Ser Met Ile Glu Gly Ala Phe Asp Leu Leu Lys Asp Glu Gly
115    120    125
Ala Leu Glu Lys Ser Asp Phe Leu Ile Ile Glu Asn Val Gly Asn Leu
130    135    140
Val Cys Pro Ser Ser Tyr Asn Leu Gly Ala Ala Met Asn Ile Val Leu
145    150    155    160
Leu Ser Val Pro Glu Gly Asp Asp Lys Val Leu Lys Tyr Pro Thr Met
165    170    175
Phe Met Cys Ala Asp Ala Val Ile Ile Ser Lys Ala Asp Met Ile Glu
180    185    190
Val Phe Asn Phe Arg Val Ser Gln Val Lys Glu Asp Met Gln Lys Leu
195    200    205
Lys Pro Glu Ala Pro Ile Phe Leu Met Ser Ser Lys Asp Pro Lys Ser
210    215    220
Leu Glu Asp Phe Lys Asn Phe Leu Leu Glu Lys Lys Arg Glu Asn Tyr
225    230    235    240
Gln Ser Thr His Ser Phe
245

```

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 957 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705

Gly Lys Ile Met Ala Lys Lys Lys Gln Glu Val Arg Asn Asn Glu Ile

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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|----|--|--|-----|--|--|--|--|--|--|--|--|--|----|--|--|-----|
| 1 | | | | | | | | | | | | | 5 | | | | | | | | | | | | | 10 | | | | | | | | | | | | | 15 | | | |
| Phe | Val | Ala | Gln | Lys | Leu | Ala | Glu | Glu | Glu | Leu | Asn | Ala | Asn | Glu | Ile | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 20 | | | | | | | | | | | | | 25 | | | | | | | | | | | | | 30 |
| Asn | Asp | Pro | Leu | Glu | Met | Leu | Asp | Phe | Lys | Ser | Phe | Asp | Asn | Asn | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 35 | | | | | | | | | | | | | 40 | | | | | | | | | | | | | 45 |
| Glu | Leu | Leu | Asp | Tyr | Gln | Gln | Gln | Ala | Leu | Ile | Asn | Ala | Phe | Arg | Val | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 50 | | | | | | | | | | | | | 55 | | | | | | | | | | | | | 60 |
| Leu | Val | Ala | Tyr | Phe | Arg | Asp | Phe | Lys | Glu | Ser | Lys | Lys | Glu | Phe | Tyr | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 65 | | | | | | | | | | | | | 70 | | | | | | | | | | | | | 75 |
| Ala | Phe | Tyr | Gln | Lys | His | Tyr | Ser | Phe | Ala | Asn | Cys | Asp | Phe | Ala | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 85 | | | | | | | | | | | | | 90 | | | | | | | | | | | | | 95 |
| Lys | Lys | Leu | Asn | His | Leu | Leu | Lys | Ser | His | Phe | Lys | Val | Glu | Asn | His | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 100 | | | | | | | | | | | | | 105 | | | | | | | | | | | | | 110 |
| Cys | Val | Arg | Phe | Glu | Asn | Phe | Ile | Asn | Arg | Leu | Ala | Phe | Tyr | Met | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 115 | | | | | | | | | | | | | 120 | | | | | | | | | | | | | 125 |
| Thr | Gly | Ser | Gly | Lys | Thr | Ile | Val | Ile | Ile | Lys | Leu | Val | Glu | Leu | Leu | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 130 | | | | | | | | | | | | | 135 | | | | | | | | | | | | | 140 |
| Ser | Val | Ala | Met | Gly | Met | Gly | Leu | Ile | Pro | Lys | Lys | Asn | Ile | Met | Phe | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 145 | | | | | | | | | | | | | 150 | | | | | | | | | | | | | 155 |
| Phe | Ser | Ala | Asn | Glu | His | Leu | Ile | Lys | Gln | Phe | Glu | Lys | Glu | Ile | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 165 | | | | | | | | | | | | | 170 | | | | | | | | | | | | | 175 |
| Lys | Tyr | Asn | Arg | Asn | Lys | Asp | Tyr | Ser | Lys | Gln | Ile | Asp | Phe | Lys | Asn | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 180 | | | | | | | | | | | | | 185 | | | | | | | | | | | | | 190 |
| Leu | Lys | Ser | Val | Lys | Asn | Lys | Asp | Phe | Tyr | Arg | Ala | Pro | Lys | Asp | Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 195 | | | | | | | | | | | | | 200 | | | | | | | | | | | | | 205 |
| Leu | Met | Lys | Glu | Ile | Ala | Leu | Phe | Tyr | Tyr | Arg | Ala | Asp | Leu | Met | Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 210 | | | | | | | | | | | | | 215 | | | | | | | | | | | | | 220 |
| Asp | Glu | Glu | Ser | Lys | Glu | Asn | Leu | Leu | Asn | Tyr | Lys | Asp | Cys | Trp | Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 225 | | | | | | | | | | | | | 230 | | | | | | | | | | | | | 235 |
| Asn | Gly | Glu | Asn | Tyr | Val | Ile | Leu | Asp | Glu | Ala | His | Lys | Gly | Asn | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 245 | | | | | | | | | | | | | 250 | | | | | | | | | | | | | 255 |
| Thr | Glu | Ser | Lys | Arg | Gln | Ala | Ile | Phe | Ser | Leu | Leu | Ser | Leu | Lys | Gly | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 260 | | | | | | | | | | | | | 265 | | | | | | | | | | | | | 270 |
| Phe | Leu | Phe | Asn | Phe | Ser | Ala | Thr | Phe | Thr | Glu | Glu | Ser | Asp | Leu | Ile | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 275 | | | | | | | | | | | | | 280 | | | | | | | | | | | | | 285 |
| Thr | Ala | Val | Tyr | Asn | Leu | Ser | Val | Gly | Glu | Trp | Val | Lys | Leu | Gly | Tyr | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 290 | | | | | | | | | | | | | 295 | | | | | | | | | | | | | 300 |
| Gly | Lys | Glu | Ser | Val | Leu | Lys | Lys | Asn | Asn | Leu | Asn | Ala | Phe | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 305 | | | | | | | | | | | | | 310 | | | | | | | | | | | | | 315 |
| Glu | Leu | Lys | Asp | Leu | Asn | Asp | Arg | Glu | Lys | Glu | Ile | Ala | Leu | Leu | Lys | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 325 | | | | | | | | | | | | | 330 | | | | | | | | | | | | | 335 |
| Ala | Leu | Leu | Leu | Leu | Gly | Met | Gln | Lys | Arg | Tyr | Lys | Val | Glu | Gly | Tyr | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 340 | | | | | | | | | | | | | 345 | | | | | | | | | | | | | 350 |
| Phe | His | Asp | Pro | Leu | Met | Leu | Val | Phe | Thr | His | Ser | Val | Asn | Met | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 355 | | | | | | | | | | | | | 360 | | | | | | | | | | | | | 365 |
| Asn | Ser | Asp | Ala | Glu | Ile | Phe | Phe | Lys | Thr | Leu | Ala | Arg | Val | Ile | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 370 | | | | | | | | | | | | | 375 | | | | | | | | | | | | | 380 |
| Asn | Asp | Asp | Glu | Ser | Asp | Phe | Ser | Lys | Ala | Lys | Asp | Asp | Leu | Leu | Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | 385 | | | | | | | | | | | | | 390 | | | | | | | | | | | | | 395 |
| Glu | Leu | Lys | Asn | Pro | Glu | Phe | Leu | Phe | Ser | Asp | Gly | Lys | Asp | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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```

Thr Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Asp
530          535          540
Ala Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu
545          550          555          560
Ser Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu
          565          570          575
Ala Ile Lys Asp Lys Leu Lys Pro Asn Ala Ala Met Leu Glu Met Leu
          580          585          590
Phe Val Ile Pro Thr Asn His Ala Ser Leu Glu Ala Ile Leu Lys Phe
          595          600          605
Gln Lys Glu Ser Glu Asn Gly Gly Glu Asn Arg Gly Pro Trp Arg Glu
610          615          620
Ile Lys Leu Glu Lys Thr Arg Ile Glu His Ala Leu Phe Val Pro Cys
625          630          635          640
Tyr Arg Lys Glu Gln Thr Asn Ala Leu Lys Ile Ser Gln Ser Ala Ser
          645          650          655
Phe Lys Met Ser Glu Lys Asn Phe Lys Asp Leu Lys Glu His Phe His
          660          665          670
Leu Met Ser Glu Lys His Phe Ile Leu Lys His Glu Ile Tyr Asp Pro
          675          680          685
Lys Asp Tyr Ala Leu Leu Lys Glu Met Ile Gln Thr Ala His Phe Lys
690          695          700
Lys Val Ser Thr Trp His Tyr Lys Asp Leu Asp Tyr Met Ile Ser Glu
705          710          715          720
Ile Lys Gly Lys Leu Tyr Pro Asn Gln Lys Val Pro Lys Asp Glu Phe
          725          730          735
Asn Ala Leu Asp Asn Glu Lys Ile Val His Phe Lys Arg Val Lys Val
          740          745          750
Lys Ala Asp Lys Lys Glu Lys Leu Ile Gln Thr Ile Gln Glu Val Lys
          755          760          765
Glu His Ala Pro Leu Asp Lys Glu Thr Leu Arg Lys Lys Ile Ala Gln
770          775          780
Gly Glu Ile Asp Pro Tyr Asp Thr Glu Lys His Lys Gln Asp Arg Thr
785          790          795          800
Phe Lys Val Gly Asp Ala Glu Leu Leu Lys Leu Lys Glu His Tyr Tyr
          805          810          815
Thr Pro Leu Ile Lys Ala Lys Asn Cys Asp Trp Leu Lys His Val Val
          820          825          830
Lys Val Lys Ser Glu Ser Asp Phe Leu Glu Glu Leu Leu Lys Ile Thr
          835          840          845
Glu Thr Leu Gln Glu Asn Tyr Asp Phe Trp Ala Phe Ser Lys Ile Asp
          850          855          860
Glu His Leu Asp Asn Leu Phe Ile Pro Tyr Ile Asp Asn Ala Thr Glu
865          870          875          880
Arg Arg Phe Phe Pro Asp Phe Ile Phe Trp Leu Gln Lys Gly Gly Thr
          885          890          895
Gln Ile Ile Cys Phe Ile Asp Pro Lys Gly Ser Lys His Thr Asp Tyr
          900          905          910
Glu His Lys Ala Asp Ala Tyr Gln Leu Phe Glu Asp Lys Val Phe Asn
          915          920          925
Pro Lys Asp Asp Pro Asn Leu Lys Ile Lys Val Val Leu Lys Phe Tyr
930          935          940
Gly Asp Lys Asp Asp Val Gly Glu Arg Tyr Arg Asp Leu
945          950          955

```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706

```

Cys Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu
1      5      10      15
Ile Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp
20      25      30
Arg Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn
35      40      45
Val Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys
50      55      60
Glu Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys
65      70      75      80
Glu Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr
85      90      95
Thr Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser
100     105     110
Val Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly
115     120     125
Leu Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly
130     135     140
Arg Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val
145     150     155     160
Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys
165     170     175
Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile
180     185     190
Gly Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly
195     200     205
Val Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys
210     215     220
Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg
225     230     235     240
His Val Phe Leu Ser Gly Val Lys Asn
245

```

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707

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```

Trp Tyr Phe Lys Lys Glu Arg Asn Pro Met Val Ile His Glu Lys Ile
1      5      10      15
Lys Ser Arg Phe Ser Arg Asn Trp Ser Leu Arg Asn Arg Gly Arg His
20      25      30
Phe Ala Ser Ser Ser Val Tyr Phe Phe Ser Leu Leu Val Ile Thr Ala
35      40      45
Val Asn Arg Ser Ser Ala Val Ala Trp Leu Leu Met Pro Glu His Leu
50      55      60
Ile Gly Trp Phe Leu Ile Ser Phe Ser Gly Glu Phe Val Ala Asp Met
65      70      75      80
Ala Phe Gly Lys Lys Ser Lys Ile Phe Lys Thr Arg Phe Gly Ile Ser
85      90      95
Ile Val Ser Gly Val Ser Leu Leu Leu Gly Ala Leu Pro Ala His Leu
100     105     110
Phe Phe Val Trp Phe Gly Phe Ile Asn Trp Trp Ala Val Phe Phe Ile
115     120     125
Glu Ala Gly Ala Asp Leu Leu Val Gly Cys Val Ile Gln Lys Ile Phe
130     135     140
Phe Gly Lys Tyr Trp Val Asp Arg Tyr Tyr
145     150

```

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708

```

Trp Ala Lys Gly Ala Gly Ala Leu Val Leu Glu Glu Tyr Glu Ser Ala
1      5      10      15
Lys Lys Arg Gly Ala Lys Ile Tyr Ala Glu Phe Ala Gly Tyr Gly Glu
20      25      30
Ser Gly Asp Ala Asn His Ile Thr Ala Pro Ala Pro Glu Gly Glu Arg
35      40      45
Ala Phe Lys Ala Met Lys Met Ala Leu Glu Met Ala Lys Val Glu Val
50      55      60
Cys Tyr Val Asn Ala His Gly Asp Lys His Ala Leu
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709

```

Thr Pro Met Gly Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile
1      5      10      15
Ala Leu Lys Asn Val Phe Gly Ser Lys Glu Lys Val Pro Pro Val Ser
      20      25      30
Ser Thr Lys Gly Gln Ile Gly His Cys Leu Gly Ala Ala Gly Ala Leu
      35      40      45
Val Ala Val Ile Ser Ile Met Ala Met Asn Gln Gly Ile Leu Pro Pro
      50      55      60
Thr Ile Asn Gln Glu Thr Pro Asp Pro Glu Cys Asp Leu Asp Tyr Ile
65      70      75      80
Pro Asn Thr Ala Arg Glu Lys Gln Val Asn Ala Val Met Ser Asn Ser
      85      90      95
Phe Gly Phe Gly Gly Thr Asn Gly Val Val Ile Phe Lys Lys Ala
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710

```

Gly Pro Ile Gln Ser Ala Pro Ala Met Asn Lys Leu Phe Leu Ala Phe
1      5      10      15
Ile Val Gly Gly Met Leu Leu Ser Ala Asp Ala Leu Asn Asp Lys Ile
      20      25      30
Glu Asn Leu Met Gly Glu Arg Ser Tyr His Met Asn Lys Leu Phe Leu
      35      40      45
Glu Arg Leu Phe Lys Asn Arg Lys Asp Phe Tyr Glu Met Gly Arg Leu
      50      55      60
Asp Ser Leu Lys Leu Leu Asn Thr Leu Lys Glu Asn Gly Leu Leu Ser
65      70      75      80
Phe Asn Phe Asp Lys Pro Ser Val Leu Lys Ile Thr Phe Lys Ala Ser
      85      90      95
Ser Asn Pro Leu Ala Phe Ala Lys Ser Ile Asn Asn Ser Leu Asn Met
      100      105      110
Met Gly Tyr Ser Tyr Val Leu Pro Ile Arg Met Gln Ser Ser Ser Gly
      115      120      125
Glu Asn Val Phe Ser Tyr Glu Leu Lys Thr Glu Tyr Val Leu Asp Pro
      130      135      140
Asn Ile Leu Ile Glu Thr Met Lys Arg His Gly Phe Asp Phe Met Asp
145      150      155      160

```

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Ile Arg Arg Val Ser Leu Lys Glu Trp Glu Tyr Asp Phe Ala Leu Gln
 165 170 175
 Lys Ile Lys Leu Pro Asn Gly Glu Ser Leu Ser Phe Glu
 180 185

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711

Met Glu Gln Asn Lys Lys Ser Leu Glu Asn Leu Asp Leu Ser Asp Val
 1 5 10 15
 Gln Asn Ile Ser Lys Asp Ile Ser Gly Thr Ala Leu Glu Glu Leu Ser
 20 25 30
 Leu Lys Asn Leu Asp Lys Asn Leu Gln Ile Leu Lys Glu Val Gly Ala
 35 40 45
 Ala Glu Ile Cys Lys Ala Thr Lys Ile Ala Ser Lys Asn Ile His Ser
 50 55 60
 Ile Leu Glu Lys Arg Tyr Glu Ser Leu Ser Arg Val His Ala Arg Gly
 65 70 75 80
 Phe Ile Gln Ile Leu Glu His Glu Tyr Lys Ile Asp Leu Ser Ala Trp
 85 90 95
 Val Lys Glu Phe Asp Lys Val Cys Val Phe Lys Glu Gly Val Gly Glu
 100 105 110
 Glu Gln Lys Gln Glu Thr Ser Pro Glu Glu Thr Ala Lys Lys Pro Leu
 115 120 125
 Lys Val Glu Leu Asp Tyr Ser Ile Asn Gln Ala Asn Thr Ser Leu Ser
 130 135 140
 Lys Lys Ser Ser Lys Trp Lys Pro Phe Val Ile Val Leu Gly Val Val
 145 150 155 160
 Val Ile Ile Leu Val Val Ile Ile Gln Asn Ser Ser Ser Leu Lys
 165 170 175
 Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys Asn Asn
 180 185 190
 Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu Pro Thr
 195 200 205
 Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly Lys Glu
 210 215 220
 Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys Arg Asp
 225 230 235 240
 Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser Phe Gln
 245 250 255
 Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His Arg Leu
 260 265 270
 Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn His Gln
 275 280 285
 Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr Glu Pro
 290 295 300
 Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala Leu Gln

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305
Gln

310

315

320

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Gly | Asn | Thr | Thr | Leu | Pro | Tyr | Lys | Arg | Ser | Ser | Ser | Leu | Thr |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Ala | Arg | Ala | Leu | Val | Leu | Ser | Ser | Asp | Pro | Val | Glu | Phe | Lys | Glu | Ala |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Ser | Gly | Lys | Tyr | Trp | Leu | Ser | Val | Asn | Gln | Asn | Ala | Tyr | Leu | Lys | Ile |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Ser | Ser | Asn | Asn | Pro | Leu | Trp | Gln | Pro | Lys | Ile | Ile | Phe | Tyr | Asp | Glu |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Asn | Leu | Lys | Ile | Ile | Gln | Ile | Ile | Ala | Lys | Glu | Asn | Arg | Gln | Gln | Glu |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ile | Ala | Leu | Asn | Leu | Leu | Asp | Gly | Val | Arg | Phe | Ile | His | Ile | Thr | Asp |
| | | 85 | | | | | | 90 | | | | | | 95 | |
| Ala | Lys | Asn | Pro | Ile | Ile | Leu | Lys | Asn | Gly | Ile | Ser | Val | Val | Phe | Asp |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Ala | Met | Pro | | | | | | | | | | | | | |
| | | 115 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Leu | Ala | Cys | Trp | Leu | Arg | Leu | Ser | Leu | Phe | Lys | Gly | Ile | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

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```

Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
    20      25      30
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
    35      40      45
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
    50      55      60
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Gln Ser
    65      70      75      80
Ile Leu Cys Leu Ile Lys Lys Glu Met Met Arg Pro Lys Gly Ile Leu
    85      90      95
Met Asn Cys Cys Arg Ala Trp Lys His Gln Val Leu Lys Gln Ser Thr
    100     105     110
Thr Gly Leu Val Val Leu Ser Ile Ile Ser Ser Thr Ala Pro Phe Ile
    115     120     125
Gly Leu Phe Gly Thr Val Val Glu Ile Leu Glu Ala Phe Asn Asn Leu
    130     135     140
Gly Ala Leu Gly Gln Ala Ser Phe Gly Val Ile Ala Pro Ile Ile Ser
    145     150     155     160
Lys Ala Leu Ile Ala Thr Ala Ala Gly Ile Leu Ala Ala Ile Pro Ala
    165     170     175
Tyr Ser Phe Tyr Leu Ile Leu Lys Arg Lys Val Tyr Asp Leu Ser Val
    180     185     190
Tyr Val Gln Met Gln Val Asp Ile Leu Ser Ser Lys Lys
    195     200     205

```

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714

```

Lys Val Phe Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu
1      5      10      15
Leu Asn Ile Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile
    20      25      30
Leu Met Val Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu
    35      40      45
Pro Ser Gly Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu
    50      55      60
Ile Arg Met Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr
    65      70      75      80
Glu Tyr Asn Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr
    85      90      95
Asp Lys Asp Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr
    100     105     110
Asp Lys Val Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu
    115     120     125
Lys Val Ser Leu Ile Thr Ser Pro
    130     135

```

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(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715

```

Lys Val Gly Pro Ile Cys Met Ser Lys Ser Ala Ile Phe Val Leu Ser
1          5          10          15
Gly Phe Leu Ala Phe Leu Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu
20          25          30
Leu Glu Arg His Asn Lys Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn
35          40          45
Lys Lys Asp Glu Gln Ala Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser
50          55          60
Glu Lys Lys Asn Glu Lys Ile Glu Lys Val Thr Glu Lys Gln Gly Asp
65          70          75          80
Phe Leu Glu Pro Lys Glu Glu Pro Lys Glu Glu Pro Glu Glu Ser Leu
85          90          95
Glu Asp Ile Phe Ser Ser Leu Asn Asp Phe Gln Glu Arg Gln Thr Lys
100          105          110
Thr Leu Lys Lys Thr Ser Lys Lys Met Asn Lys Lys Asn Lys Gly Val
115          120          125

```

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716

```

Gly Arg Thr Met Lys Tyr Leu Trp Leu Phe Leu Ile Tyr Ala Ile Gly
1          5          10          15
Leu Phe Ala Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gln Lys
20          25          30
Leu Pro Lys Ile Glu Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr
35          40          45

```

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```

Ala Leu Lys Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln
 50          55          60
His Phe Asp Val Ser Gln Asn Lys Glu Gln Gly Ala Ile Asn Tyr Ala
 65          70          75          80
Glu Leu Lys Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala
          85          90          95
Val Glu Asn Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp
          100          105          110
Thr Gly Thr Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp
          115          120          125
Leu Tyr Pro Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr
          130          135          140
Leu Lys Ala Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser
          145          150          155          160
Lys Tyr Ile Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asp Tyr Thr
          165          170          175
Met Arg Tyr Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe
          180          185          190
Pro Lys Trp Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr Thr Gln Met
          195          200          205
Ala Glu Lys Arg Pro Trp Phe
          210          215

```

(2) INFORMATION FOR SEQ ID NO:1717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717

```

Phe Leu Arg Gly Lys Phe Ile Gln Glu Arg Leu Lys Ala Leu Cys Cys
 1          5          10          15
Gln Gly Val Glu Gly Glu Phe Gly Val Leu Tyr Gly His Ser Asn Met
          20          25          30
Ile Thr Leu Leu Gln Ala Gly Val Val Glu Ile Glu Thr Glu Asn Gln
          35          40          45
Lys Glu His Ile Ala Ile Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu
          50          55          60
Arg Val Asp Ile Leu Ala Asp Gly Ala Val Phe Ile Lys Lys Gly Ser
          65          70          75          80
Asp Asp Arg Asp Asp Ala Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp
          85          90          95
Ala Ser Ser Asp Arg Leu Ala Val Ser Ser Val Leu Ala Lys Ile Glu
          100          105          110
Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:1718:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718

```

Lys Leu Ser Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser
1          5          10          15
Lys Arg Ile Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met
          20          25          30
Leu Ala Tyr Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys
          35          40          45
Val Phe Ile Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn
          50          55          60
Tyr Gly Ala Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Glu
65          70          75          80
Gln Gly His Asp Phe Arg Ser Asp Gly Leu Ser His Glu Arg Ile Arg
          85          90          95
Ile Lys Arg
  
```

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719

```

Ile Pro Pro Ser Thr Pro Phe Leu Asn Ile Leu His Val Phe Lys His
1          5          10          15
Tyr Arg Ser His Tyr Gly Lys Ile Asn Thr Cys Leu Asn Thr Leu Gly
          20          25          30
Asp Leu Ile Leu Ala Leu Pro Val Tyr Tyr Asp Lys Asp Ile Asp Leu
          35          40          45
Gly Val Ile Gln Ser Leu Gln Val Gly Ile Ile Gly Tyr Gly Val Gln
          50          55          60
Gly Glu Ala Gln Ala Leu Asn Leu Arg Asp Ser Lys Val Lys Val Arg
65          70          75          80
Ile Gly Leu Tyr Gln Gly Ser Leu Ser Val Ser Lys Ala Lys Lys Glu
          85          90          95
  
```

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```

Gly Phe Glu Val Leu Gly Val Lys Glu Leu Val Gln Gln Ser Asp Val
      100      105      110
Ile Met Ala Leu Leu Pro Asp Glu Leu His Lys Glu Val Leu Glu Lys
      115      120      125
Glu Val Ile Pro Phe Leu Lys Glu Gly Gln Ile Ile Gly Phe Ala His
      130      135      140
Gly Phe Ser Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly
145      150      155      160
Ala Ile Leu Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Glu Glu
      165      170      175
Tyr Leu Lys Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Glu Gln Glu
      180      185      190
Ser Ser Ile His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala
      195      200      205
Met Gly Gly Gly Arg Met Gly Val Leu Glu Thr Ser Phe Lys Glu Glu
      210      215      220
Cys Glu Ser Asp Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Leu
225      230      235      240
Glu Ala Ile Val Arg Met Gly Phe Glu Thr Leu Ile Lys Ala Gly Tyr
      245      250      255

```

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720

```

Gln Thr Ser Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His Met Lys
1      5      10      15
Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val
      20      25      30
Ser Val Phe Leu Gln Glu Lys His Leu Gln Asn Ala Phe Glu Thr Leu
      35      40      45
Lys Gln Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser
50      55      60
Ala Ser Pro Ile Val Leu Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu
65      70      75      80
Leu Lys Ser Ile Gln Thr Arg Ala Arg Lys Ile
      85      90

```

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721

```

Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr
1      5      10      15
Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile
20      25      30
Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp
35      40      45
Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser
50      55      60
Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val
65      70      75      80
Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val
85      90      95
Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp
100      105      110
Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val
115      120      125
Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser
130      135      140
Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe
145      150      155      160
Asn Ala Leu Leu Lys Pro Lys Val Pro Pro Tyr Tyr Pro Phe Cys Leu
165      170      175
Pro Ser Gly Leu Tyr Arg Glu Asn Ile Lys Ser Tyr Lys Glu Ala His
180      185      190
Leu Val Ile Thr Glu Asp Lys Asp Tyr Gln Arg Ile Thr Ser Ile Thr
195      200      205
Asn Pro Thr Lys Arg Met Leu Leu Val Thr Ala Ile Ala Asn Pro Ser
210      215      220
Arg Leu Asp Ala Phe Leu Pro Lys Glu Val Val Lys Lys Leu Tyr Phe
225      230      235      240
Arg Asp His Ala Pro Phe Asp Leu Lys Leu Leu Glu Lys Glu Phe Tyr
245      250      255
Gln Asn Asn Ala Thr Ser Leu Leu Val Thr Ser Lys Asp Leu Val Lys
260      265      270
Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
275      280      285
Ile Cys Pro Lys Val Leu Glu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
290      295      300
Pro Cys Asn Ile Lys Glu His Leu
305      310

```

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722

```

Lys Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser
1      5      10      15
Leu Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala
20      25      30
Asn Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly
35      40      45
Leu Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe
50      55      60
Glu Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val
65      70      75      80
Phe Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys
85      90      95
Ile Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser
100      105      110
Thr Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr
115      120      125
Phe Ile Ala Phe Leu Phe Ala Ile Phe Met Leu Val Gly Ile Ser Asn
130      135      140
Ala Ile Asn Ile Ile Asp Gly Phe Asn Gly Leu Ala Ser Gly Ile Cys
145      150      155      160
Ala Ile Ala Leu Leu Val Ile His Tyr Ile Asp Pro Ser Ser Leu Ser
165      170      175
Cys Leu Leu Ala Tyr Met Val Leu Gly Phe Met Val Leu Asn Phe Pro
180      185      190
Ser Gly Lys Ile Phe
195

```

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723

```

Gln Phe Val Leu Phe Ala Arg Leu His Gly Ala Trp Val Tyr Gly Val
1      5      10      15
Lys Phe Pro Phe Arg Lys Asp Phe Leu Gly Asp Gly Gly Ala Tyr Phe
20      25      30
Leu Gly Leu Val Cys Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
35      40      45
Lys Ile Ser Val Phe Phe Gly Leu Asn Leu Met Leu Tyr Pro Val Ile
50      55      60
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala

```

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```

65          70          75          80
Thr Met Pro Asp Asn Leu His Leu His Thr Leu Leu Phe Lys Phe Leu
          85          90          95
Gln Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu
          100          105          110
Ile Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu
          115          120          125
Asp Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Ala Cys Tyr
          130          135          140
Leu Ile Gly Tyr Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys
145          150          155          160
Arg Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724

```

Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1          5          10          15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys
          20          25          30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
          35          40          45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
          50          55          60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
65          70          75          80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
          85          90

```

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725

```

Val Lys Lys Ser Asn Asn Met Val Val Glu Leu Lys Asn Ile Glu Lys
1      5      10      15
Ile Tyr Glu Asn Gly Phe His Ala Leu Lys Gly Val Asn Leu Glu Leu
20      25      30
Lys Lys Gly Asp Ile Leu Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys
35      40      45
Ser Thr Leu Ile Arg Leu Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly
50      55      60
Glu Val Leu Val Asn Gly Val Asn Leu Leu Asn Leu Lys Pro Lys Glu
65      70      75      80
Leu Gln Lys Ala Arg Gln Lys Ile Gly Met Ile Phe Gln His Phe Asn
85      90      95
Leu Leu Ser Ala Lys Asn Val Phe Glu Asn Val Ala Phe Ala Leu Glu
100     105     110
Ile Ala Arg Trp Glu Lys Thr Lys Ile Lys Ser Arg Val His Glu Leu
115     120     125
Leu Glu Leu Val Gly Leu Glu Asp Lys Val His Phe Tyr Pro Lys Gln
130     135     140
Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu Ala
145     150     155     160
Asn Cys Pro Asn Leu Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp
165     170     175
Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys
180     185     190
Lys Phe Asp Leu Ser Ile Val Phe Ile Thr His Gln Ile Glu Val Val
195     200     205
Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile Val
210     215     220
Glu Arg Gly Ser Val Glu Glu Ile Phe Ala Asn Pro Lys His Ala Val
225     230     235     240
Thr Lys Glu Leu Leu Gly Ile Lys Asn Glu His Ala Asp Gln Lys Ser
245     250     255
Gln Asp Ile Tyr Arg Ile Val Phe Leu Gly Glu His Leu Asp Glu Pro
260     265     270
Ile Ile Ser Asn Leu Ile Arg Arg Phe Lys Ile Arg Arg
275     280     285

```

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726

```

Leu Phe Cys Ser Cys Leu Tyr Gln Arg Phe Leu Ile Gly Thr Ser Ile
1      5      10      15
Gly Ser Ser Ala Ser Ile Ile Pro Leu Ala Ile Ser Ala Ile Pro Phe

```

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```

      20      25      30
Val Val Lys Leu Phe Glu Asn Ser Leu Met Glu Val Glu His Gly Lys
      35      40      45
Ile Glu Thr Thr Leu Ser Leu Gly Ala Ser His Leu Glu Val Ile Lys
      50      55      60
Met Met Leu Leu Glu Ser Leu Pro Ser Leu Val Asn Asn Ile Thr Ile
      65      70      75      80
Thr Leu Ile Ser Leu Ile Gly Tyr Ser Ala Met Ala Gly Ala Leu Gly
      85      90      95
Ala Gly Gly Leu Gly Asp Leu Ala Ile Arg Ile Gly Tyr Gln Ser Tyr
      100      105      110
Arg Gly Asp Val Leu Phe Tyr Ala Val Val Val Ile Ile Val Leu Val
      115      120      125
Gln Ile Ile Gln Ser Ala Gly Asp Tyr Val Val Lys Arg Leu Arg Lys
      130      135      140
Asn Lys Tyr
145

```

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727

```

Ser Tyr Phe Cys Tyr Asn Leu Arg Leu Leu Ser Leu Val Lys Gly Lys
1      5      10      15
Thr Met Leu Arg Ser Leu Tyr Ser Ala Thr Ser Gly Met Leu Ala Gln
      20      25      30
Gln Thr His Ile Asp Thr Thr Ser Asn Asn Ile Ala Asn Val Asn Thr
      35      40      45
Thr Gly Phe Lys Lys Ser Arg Ala Asp Phe Asn Asp Leu Phe Tyr Gln
      50      55      60
Ala Met Gln Tyr Ala Gly Thr Asn Thr Ser Asn Thr Thr Leu Ser Pro
      65      70      75      80
Asp Gly Met Glu Val Gly Leu Gly Val Arg Pro Ser Ala Ile Thr Lys
      85      90      95
Met Phe Ser Gln Gly Ser Pro Lys Glu Thr Glu Asn Asn Leu Asp Ile
      100      105      110
Ala Ile Thr Gly Lys Gly Phe Phe Gln Val Gln Leu Pro Asp Gly Thr
      115      120      125
Thr Ala Tyr Thr Arg Ser Gly Asn Phe Lys Leu Asp Glu Gln Gly Asn
      130      135      140
Leu Val Thr Ser Glu Gly Tyr Leu Leu Ile Pro Gln Ile Thr Leu Pro
      145      150      155      160
Glu Asp Thr Thr Gln Val Asn Ile Gly Val Asp Gly Thr Val Ser Val
      165      170      175
Thr Gln Gly Leu Gln Thr Thr Ser Asn Val Ile Gly Gln Ile Thr Leu
      180      185      190
Ala Asn Phe Val Asn Pro Ala Gly Leu His Ser Met Gly Asp Asn Leu
      195      200      205

```

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```

Phe Ser Ile Thr Asn Ala Ser Gly Asp Ala Ile Val Gly Asn Pro Asp
210                215                220
Ser Gln Gly Leu Gly Lys Leu Arg Gln Gly Phe Leu Glu Leu Ser Asn
225                230                235                240
Val Arg Leu Val Glu Glu Met Thr Asp Leu Ile Thr Ala Gln Arg Ala
                245                250                255
Tyr Glu Ala Asn Ser Lys Ser Ile Gln Thr Ala Asp Ala Met Leu Gln
                260                265                270
Thr Val Asn Ser Leu Lys Arg
                275

```

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728

```

Lys Trp Arg Asn Ser Ser Ser Asp Lys Met Ala Lys Lys Lys Ile Ala
1                5                10                15
Ile Ser Cys Gly Asp Ile Gln Gly Val Gly Leu Glu Leu Ile Leu Lys
                20                25                30
Ser His Lys Glu Val Ser Ala Leu Cys Glu Pro Leu Tyr Leu Val His
35                40                45
Ser Glu Leu Leu Glu Arg Ala Asn Gln Leu Leu Asp Asn Ala Tyr Glu
50                55                60
Thr Lys Thr Leu Asn Ala Ile Ala Ile Asp Ala Pro Leu Pro Leu Leu
65                70                75                80
Asn Ser Ser Thr Ile Gly Lys Val Ser Thr Gln Ser Gly Ala Tyr Ser
85                90                95
Phe Glu Ser Phe Lys Lys Ala Cys Glu Leu Ala Asp Ser Lys Glu Val
100                105                110
Asp Gly Ile Cys Thr Leu Pro Ile Asn Lys Leu Ala Trp Gln Gln Ala
115                120                125
Gln Ile Pro Phe Val Gly His Thr Asp Phe Leu Lys Gln Arg Tyr Lys
130                135                140
Asp His Gln Ile Ile Met Met Leu Gly Cys Ser Lys Leu Phe Val Gly
145                150                155                160
Leu Phe Ser Asp His Val Pro Leu Ser Ala Val Ser Gln Leu Ile Gln
165                170                175
Val Lys Ala Leu Val Lys Phe Leu Leu Ala Phe Gln Lys Ser Thr Gln
180                185                190
Ala Lys Ile Val Gln Val Cys Gly Phe Asn Pro His Ala Gly Glu Glu
195                200                205
Gly Leu Phe Gly Glu Glu Asp Glu Lys Ile Leu Lys Ala Ile Gln Glu
210                215                220
Ser Asn Gln Thr Leu Gly Phe Glu Cys Phe Leu Gly Pro Leu Pro Ala
225                230                235                240
Asp Ser Ala Phe Ala Pro Asn Lys Arg Lys Ile Thr Pro Phe Tyr Val
245                250                255
Ser Met Ser His Asp Val Gly Leu Ala Pro Leu Lys Ala Leu Tyr Phe

```

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```

      260      265      270
Asp Glu Ser Ile Asn Val Ser Leu Asn Ala Pro Ile Leu Arg Ala Ser
      275      280      285
Thr Asp His Gly Thr Ala Phe Asp Ile Ala Tyr Gln Asn Lys Ala Asn
      290      295      300
His Lys Ser Tyr Leu Asn Ala Ile Lys Tyr Leu Ala
305      310      315

```

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729

```

Gln Gly Ile Ile Gln Ala Lys Thr Pro Pro Lys Asp Lys Asp Met Ile
1      5      10      15
Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg
      20      25      30
Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln Glu Lys
      35      40      45
His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser Arg Leu
      50      55      60
His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile Ser Leu
      65      70      75      80
Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn Gln Pro
      85      90      95
Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys Ala Leu
      100      105      110
Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu Arg Gly
      115      120      125
His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met Pro Leu
      130      135      140
Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu Ala Arg
      145      150      155      160
Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp Ser Phe
      165      170      175
Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly Tyr Pro
      180      185      190
Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His Pro Asn
      195      200      205
Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn Leu Ala
      210      215      220
Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val Glu Lys
      225      230      235      240
Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly Tyr His
      245      250      255
Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys Arg Tyr
      260      265      270
Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly Ala Ser
      275      280      285

```

SUBSTITUTE SHEET (RULE 26)

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Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala Glu Phe
 290 295 300
 Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp Asn Ala
 305 310 315 320
 Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe
 325 330 335
 Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu Lys Asn
 340 345 350
 Phe Glu

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730

Arg Asn Asn Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys
 1 5 10 15
 Gln Leu Glu Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe
 20 25 30
 Gly Lys Asp Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile
 35 40 45
 Glu Tyr Lys Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile
 50 55 60
 Ala Glu Glu Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile
 65 70 75 80
 Lys Gly Glu Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp
 85 90 95
 Lys Leu Lys Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu
 100 105 110
 Gln Asn Met Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp
 115 120 125
 Asp Glu Glu Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr
 130 135 140
 Asp Asn Leu Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe
 145 150 155 160
 Lys Met Gly Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn
 165 170 175
 Ala Val Ala Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn
 180 185 190
 Gln Val Leu Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp
 195 200 205
 Ile Ile Thr Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr
 210 215 220
 Arg Val Thr Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys
 225 230 235 240
 Thr Gln Gln Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
 245 250 255

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(2) INFORMATION FOR SEQ ID NO:1731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...101
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731

```

Val Ile Ile Phe Leu Leu Leu Phe Phe Leu Gly Asn Lys Val Phe Ser
1           5           10           15
Ile Tyr Leu Leu Leu Glu Ser Phe Leu Trp Val Ile Leu Thr Thr Trp
          20           25           30
Cys Cys Leu Val Met His Glu Asp Gln Arg Gln Lys Asp Met Glu Gln
          35           40           45
Leu Ile Asn Gly Ile Asp Arg Ile Ile Lys Ala Asn Ser Gly Lys Ser
          50           55           60
Leu His Gln Glu Thr Gln Gln Ala Asn Lys Thr Asp Lys Ala Trp Asp
65           70           75           80
Leu Ala Ala Asn Val Phe Leu Ile Gly Leu Val Val Leu Ala Val Phe
          85           90           95
His Met Ile Lys Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:1732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...118
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732

```

Ala Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile
1           5           10           15
Met Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln
          20           25           30
Thr Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr
          35           40           45
Asp Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser
          50           55           60

```

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1271

```

Asn Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn
65          70          75          80
Leu Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Leu
          85          90          95
Gln Gly Asp Lys Lys Ser Asn Leu Asp Asn Phe Ile Lys Val Val Asp
          100          105          110
Leu Leu Gln Leu Thr Ile
          115

```

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733

```

Leu His Arg Gln Ala Gln Val Arg Ile Ser Leu Thr Gln Thr Thr Thr
1          5          10          15
Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu Leu Gly
          20          25          30
Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser Ala Ser
          35          40          45
Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala Leu Lys
          50          55          60
Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val Ile Tyr
65          70          75          80
Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp Asp Ile
          85          90          95
Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser Lys Ala
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734

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1272

```

Asn His Lys Ile Arg Gly Tyr Glu Lys Arg Met Ala Leu Asp Lys Arg
1      5      10      15
Ile Trp Met His Phe Asp Leu Leu Pro Phe Val Phe Ile Ile Pro Leu
20      25      30
Leu Val Val Ser Phe Leu Leu Ile Phe Glu Ser Ser Ala Val Leu Ser
35      40      45
Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly Phe Leu Leu Phe Trp Val
50      55      60
Val Phe Phe Ile Pro Phe Arg Lys Leu Asp Arg Trp Leu Phe Ala Leu
65      70      75      80
Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu Val Asp Phe Met Gly Ser
85      90      95
Ser Lys Leu Gly Ala Gln Arg Trp Leu Val Ile Pro Phe Thr Ser Ile
100     105     110
Thr Leu Gln Pro Ser Glu Pro Val Lys Ile Ala Ile Leu Leu Leu Leu
115     120     125
Ala Arg Phe Asp Gln Asn Gln Pro Thr Ser Phe
130     135

```

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735

```

Phe Cys Gly Thr Leu Lys Ala Leu Lys Ile Lys Ile Thr Thr Thr Pro
1      5      10      15
Cys Lys Ala Leu Lys Lys Lys Trp Lys Ile Leu Leu Lys His Leu Met
20      25      30
Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu Leu
35      40      45
Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His Trp
50      55      60
Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala Gly
65      70      75      80
Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp Gly
85      90      95
Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala Phe
100     105     110
Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu Val
115     120     125
Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys Arg
130     135     140
His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln Ala
145     150     155     160
Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala Ala
165     170     175
Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala Ile
180     185     190

```

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1273

Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe Gly
 195 200 205
 Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu Leu
 210 215 220
 Gly Val Thr Ala Val Ala Gln Val Gly Arg Thr Leu Val Asn Gly Phe
 225 230 235 240
 Leu Lys Phe Ile Pro Val Val Gly Ser Val Ala Gly Gly Ala Thr Ala
 245 250 255
 Ala Val Ile Thr Glu Gly Ile Gly Phe Ala Tyr Leu Lys Val Leu Glu
 260 265 270
 Lys Cys Phe Asn Asp Glu Thr Gly Glu Val Asn Leu Pro Gly Glu Val
 275 280 285
 Gly Met Ile Thr Ser Leu Phe Lys Glu Asn Tyr Leu Asn Leu Asp Thr
 290 295 300
 Ile Lys Lys Leu Lys Pro
 305 310

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736

Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
 1 5 10 15
 Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
 20 25 30
 Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
 35 40 45
 Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
 50 55 60
 Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
 65 70 75 80
 Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
 85 90 95
 Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
 100 105 110
 Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
 115 120 125
 Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu
 130 135 140
 Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp
 145 150 155 160
 Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln
 165 170 175
 Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu
 180 185 190
 Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg
 195 200 205
 Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser

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```

      210              215              220
Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn
225              230              235              240
Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp
      245              250              255
Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn
      260              265              270
Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser
      275              280              285
Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val
      290              295              300
Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro
305              310              315              320
Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys
      325              330              335
Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro
      340              345              350
Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser
      355              360              365
Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp
      370              375              380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val
385              390              395              400
Asp Lys Asp Gly Leu Glu Ser His Pro Ser Lys Glu Val Arg Leu Phe
      405              410              415
Leu Glu Arg

```

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737

```

Leu Lys Asn Thr Leu Lys Gly Leu Leu Met Leu Asp Phe Asp Leu Val
1              5              10              15
Leu Phe Gly Ala Thr Gly Asp Leu Ala Met Arg Lys Leu Phe Val Ser
      20              25              30
Leu Tyr Glu Ile Tyr Ile His Tyr Gly Phe Lys Asn Asp Ser Arg Ile
      35              40              45
Ile Ala Ser Gly Arg Lys Glu Leu Ser Asn Glu Glu Phe Leu Ala Leu
      50              55              60
Leu Cys Glu Lys Thr Gln Leu His Ser Arg Glu Lys Gly Glu Glu Phe
65              70              75              80
Leu Thr His Ile Ser Tyr Leu Arg Val Arg Leu Asp Asn Pro Lys Asp
      85              90              95
Phe Glu Glu Leu Ser Lys Ile Ala Thr Asn Asn Lys Pro Leu Ile Phe
      100              105              110
Tyr Phe Ser Ile Ser Pro Ser Phe Ala Thr Thr Ala Gln Asn Leu
      115              120              125

```

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Ala Gln Asn Ala Leu Asn His Ala Asn Thr Arg Leu Ile Leu Glu Lys
 130 135 140
 Pro Leu Gly His Asp Leu Lys Thr Cys Lys Glu Ile Phe Gln Ser Ile
 145 150 155 160
 Ser Ala Phe Phe Lys Glu Glu Gln Ile Phe Arg Ile Asp His Tyr Leu
 165 170 175
 Gly Lys Lys Gly Val Gln Asn Ile Leu Glu Leu Arg Leu Asn Asn Pro
 180 185 190
 Ile Leu Asn Ile Leu Trp Asp Gln Ile Ser Ala Val Glu Ile Cys Val
 195 200 205
 Tyr Glu Thr Leu Gly Val Glu Glu Arg Gly Glu Phe Tyr Asp Lys Ile
 210 215 220
 Gly Ala Leu Arg Asp Met Val Gln Asn His Leu Leu Gln Val Leu Ser
 225 230 235 240
 Leu Ile Ala Thr Asp Leu Pro Asn Asp Leu Lys Asp Leu Arg Gln Glu
 245 250 255
 Lys Ser Lys Phe
 260

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738

Gly Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe
 1 5 10 15
 Ser Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Ile
 20 25 30
 Ser Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu
 35 40 45
 Val Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Thr Phe Phe Ile Leu
 50 55 60
 Pro Ile Thr Phe Phe Ala Ala Cys Ala Leu Gly Leu Ser Arg Leu Ser
 65 70 75 80
 Tyr Asp His Glu Leu Val Phe Phe Ser Leu Gly Val Ser Pro Lys
 85 90 95
 Lys Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile
 100 105 110
 Leu Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr
 115 120 125
 Tyr Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg
 130 135 140
 Ala Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp
 145 150 155 160
 Lys Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys
 165 170 175
 Ser Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn
 180 185 190
 Asn Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr

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```

      195              200              205
Phe Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His
  210              215              220
Leu Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu
  225              230              235              240
Gln Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn
      245              250              255
Ala Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser
      260              265              270
Leu Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala
      275              280              285
Asn Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe His Val Leu Gly Ala
      290              295              300
Val Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe
  305              310              315              320
Leu Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu
      325              330              335
Leu Phe Arg Lys Phe Ile Leu Lys Arg Tyr
      340              345

```

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739

```

Ile Leu Ile Glu Gly Val Phe Met Pro Lys His Ser Leu Glu Gln Ile
  1              5              10              15
Lys Glu Lys Ile Thr Glu Arg Ser Lys Lys Thr Arg Glu Leu Tyr Leu
      20              25              30
Glu Asn Thr Phe Asn Pro Lys Asn Gln Pro Lys Ile Glu Ser Leu Gly
      35              40              45
Cys Ala Asn Ile Ala His Val Thr Ala Ser Met Pro Glu His Leu Lys
      50              55              60
Met Pro Leu Gly Ser His Lys Arg Lys His Phe Ala Ile Ile Thr Ala
      65              70              75              80
Tyr Asn Asp Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp
      85              90              95
Leu Ile Lys Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala
      100              105              110
Ser Gly Val Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly
      115              120              125
Met Glu Leu Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Ala
      130              135              140
Val Gly Leu Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val
      145              150              155              160
Cys Asp Lys Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly
      165              170              175
Asn Leu Ala Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile
      180              185              190

```

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Glu Asn Tyr Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys
 195 200 205
 Ile Asn Arg Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp
 210 215 220
 Val Gly Thr Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met
 225 230 235 240
 Met Glu Phe Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro
 245 250 255
 Asn Asn Pro Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu
 260 265 270
 Ala Ser Gly Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser
 275 280 285
 Ile Leu Asn Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn
 290 295 300
 His Thr Leu His Leu Ile Ala Ile Ala Arg Ser Cys Gly Val Ile Leu
 305 310 315 320
 Asn Trp Asp Asp Phe Asp Ala Ile Ser Asn Leu Ile Pro Leu Leu Ala
 325 330 335
 Lys Val Tyr Pro Asn Gly Ser Ala Asp Val Asn Ala Phe Glu Ala Cys
 340 345 350
 Gly Gly Leu Ala Phe Val Ile Lys Glu Leu Leu Lys Glu Gly Leu Leu
 355 360 365
 Phe Glu Asp Thr His Thr Ile Met Asp Thr Glu Thr Gln Lys Gly Met
 370 375 380
 Gln Asn Tyr Thr Lys Thr Pro Phe Leu Glu Asn Asp Gln Leu Val Tyr
 385 390 395 400
 Lys Asp Ala Val Ser His Ser Leu Asn Thr Asp Ile Leu Arg Pro Val
 405 410 415
 Ser Glu Pro Phe Ala Ala Asn Gly Gly Leu Lys Ile Leu Lys Gly Asn
 420 425 430
 Leu Gly Arg Ala Val Ile Lys Ile Ser Ala Ile Lys Asp Glu His Arg
 435 440 445
 Lys Val Lys Ala Arg Ala Ile Val Phe Lys Thr Gln Ser Glu Phe Leu
 450 455 460
 Glu Arg Phe Lys Asn Lys Glu Leu Glu Arg Asp Phe Val Ala Val Leu
 465 470 475 480
 Pro Phe Gln Gly Pro Lys Ser Asn Gly Met Pro Glu Leu His Lys Leu
 485 490 495
 Thr Thr Asn Leu Gly Ala Leu Gln Asp Met Gly Tyr Lys Val Ala Leu
 500 505 510
 Val Thr Asp Gly Arg Met Ser Gly Ala Ser Gly Lys Val Pro Ser Ala
 515 520 525
 Ile His Leu Ser Pro Glu Gly Ala Leu Asn Gly Ala Ile Ile Lys Ile
 530 535 540
 Lys Asp Gly Asp Leu Ile Glu Leu Asp Ala Pro Asn Asn Ala Leu Asn
 545 550 555 560
 Val Leu Glu Lys Asp Phe Glu Lys Arg Gly Ile Asn Pro Leu Phe Leu
 565 570 575
 Glu Thr Leu Glu Asn Leu Glu Lys Pro Thr Phe Gly Leu Gly Arg Glu
 580 585 590
 Leu Phe Thr Ser Leu Arg Leu Asn Ala Asn Thr Ala Glu Glu Gly Gly
 595 600 605
 Met Ser Phe Gly Ile Lys Val
 610 615

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740

```

Lys Tyr Lys Gly Asp Lys Met Gln Asp Lys Ile Ile Glu Ile Leu Gln
1      5      10      15
Ile Ser Pro Ile Val Pro Val Val Val Val Glu Asn Ile Lys Asp Ala
      20      25      30
Val Pro Leu Ala Gln Ser Leu Ile Glu Gly Gly Ile Pro Ile Ile Glu
      35      40      45
Val Thr Leu Arg Ser Asn Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala
      50      55      60
Lys Asn Val Pro Lys Met Arg Val Gly Ala Gly Thr Ile Leu Asn Leu
      65      70      75      80
Thr Gln Leu Glu Gln Ala Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser
      85      90      95
Pro Gly Leu Thr Ile Lys Leu Leu Glu His Ala Lys Lys Lys Asp Met
      100      105      110
Pro Leu Ile Pro Gly Val Ser Ser Ser Ser Glu Val Met Gln Ala Leu
      115      120      125
Glu Leu Gly Tyr Asn Ala Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly
      130      135      140
Gly Val Lys Leu Leu Asn Ala Phe Asn Gly Pro Phe Lys Gly Val Lys
      145      150      155      160
Phe Cys Pro Thr Gly Gly Ile Ser Ala Asp Asn Met Arg Ser Tyr Leu
      165      170      175
Ala Leu Glu Asn Val Val Cys Val Gly Gly Ser Trp Leu Thr Pro Lys
      180      185      190
Asp Leu Ile Gln Asn Lys Glu Trp Asp Lys Ile Thr Glu Ile Cys Lys
      195      200      205
Arg Ala Leu Ala Leu Arg
      210

```

(2) INFORMATION FOR SEQ ID NO:1741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741

```

Asn Thr Ala Ile Val Ser Phe Leu Trp Phe Ala Tyr Val Ser Ile Gly
1      5      10      15
Leu Thr Asn Phe Val Ala Val Gly Tyr Met Val Ser Leu Leu Gly Ala
      20      25      30

```

SUBSTITUTE SHEET (RULE 26)

1279

Leu Lys Arg Thr Pro Cys Thr Asn Arg Phe Tyr Leu Lys Ala Leu Leu
 35 40 45
 Phe Ala Ile Phe Tyr His Ala Val Asn Asn Phe Leu Thr Gln Cys Pro
 50 55 60
 Pro His Gln Val Arg Glu Phe Phe Ser Ser Arg His Ala Gln Gly Trp
 65 70 75 80
 Lys Arg Glu Thr Leu Pro Cys Ala Leu Ser Phe Gln Asn Ala Leu
 85 90 95

(2) INFORMATION FOR SEQ ID NO:1742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742

Lys Lys Thr Pro Pro Ile Leu Cys Arg Leu Leu Gly Phe Tyr Ile Leu
 1 5 10 15
 Lys Lys Leu Pro Gln Arg Cys Phe Met Pro Lys Thr Glu Thr Tyr Pro
 20 25 30
 Arg Leu Leu Ala Asp Ile Gly Gly Thr Asn Ala Arg Phe Gly Leu Glu
 35 40 45
 Val Ala Pro Arg Gln Ile Glu Cys Val Glu Val Leu Arg Cys Glu Asp
 50 55 60
 Phe Glu Ser Leu Ser Asp Ala Val Arg Phe Tyr Leu Ser Lys Cys Lys
 65 70 75 80
 Glu Ser Leu Lys Leu His Pro Ile Tyr Gly Ser Phe Ala Val Ala Thr
 85 90 95
 Pro Ile Met Gly Asp Phe Val Gln Met Thr Asn Asn His Trp Thr Phe
 100 105 110
 Ser Ile Glu Thr Thr Arg Gln Cys Leu Asn Leu Lys Lys Leu Leu Val
 115 120 125
 Ile Asn Asp Phe Val Ala Gln Ala Tyr Ala Ile Ser Ala Met Gln Glu
 130 135 140
 Asn Asp Leu Ala Gln Ile Gly Gly Ile Lys Cys Glu Ile Asn Ala Pro
 145 150 155 160
 Lys Ala Ile Leu Gly Pro Gly Thr Gly Leu Gly Val Ser Thr Leu Ile
 165 170 175
 Gln Asn Ser Asp Gly Ser Leu Lys Val Leu Pro Asp Glu Gly Gly His
 180 185 190
 Val Ser Phe Ala Pro Phe Asp Asp Leu Glu Ile Leu Val Trp Gln Tyr
 195 200 205
 Ala Arg Ser Lys Phe Asn His Val Ser Ala Glu Arg Phe Leu Ser Gly
 210 215 220
 Ser Gly Leu Val Leu Ile Tyr Glu Ala Leu Ser Lys Arg Lys Gly Leu
 225 230 235 240
 Glu Lys Val Ala Lys Leu Ser Lys Ala Glu Leu Thr Pro Gln Ile Ile
 245 250 255
 Ser Glu Arg Ala Leu Asn Gly Asp Tyr Pro Ile Cys Arg Leu Thr Leu
 260 265 270
 Asp Thr Phe Cys Ser Met Leu Gly Thr Leu Ala Ala Asp Val Ala Leu

SUBSTITUTE SHEET (RULE 26)

1280

```

      275              280              285
Thr Leu Gly Ala Arg Gly Gly Val Tyr Leu Cys Gly Gly Ile Ile Pro
290              295              300
Arg Phe Ile Asp Tyr Phe Lys Thr Ser Pro Phe Arg Ala Arg Phe Glu
305              310              315
Thr Lys Gly Arg Met Gly Ala Phe Leu Ala Ser Ile Pro Val His Val
325              330              335
Val Met Lys Lys Thr Pro Gly Leu Asp Gly Ala Gly Ile Ala Leu Glu
340              345              350
Asn Tyr Leu Leu His Asp Arg Ile
355              360

```

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743

```

Ser Gln Gly Leu Ile Phe Asp Lys Lys Lys Gln Lys Phe Leu Lys Asp
1              5              10              15
Phe Lys Ala Gly Glu Leu Leu Tyr Gln Ser His Phe Lys Pro Leu Val
20              25              30
Glu Phe Ile Ala Glu Glu Leu Leu Lys Asn Ser Arg Ala Lys Ile Ile
35              40              45
Gln Ser Asn Cys Asn Lys Ala Leu Lys Val Val Glu Glu Leu Gln Asn
50              55              60
Thr Ile Lys Thr Thr Ile Glu Lys Gln Ile Asn Pro Gly Met Lys Glu
65              70              75              80
Thr Gln Asp Pro Gln Gln Glu Ala Arg Phe Asn Leu Asp Arg Ser Thr
85              90              95
Asp Lys Phe Ile Ser Asp Leu Glu Lys Ser Ala Phe Ser Lys Ile Asn
100             105             110
Gln Phe Glu Phe Asn Phe Arg Lys Glu Met His Glu Arg Ile Glu Arg
115             120             125
Gly Ile Gly Asn Asn Glu Cys Lys Glu Ile Phe Gly Asn Glu Leu Lys
130             135             140
Gln Arg Lys Thr Lys Leu Ile Glu Asp Ile Glu Arg Arg Phe Lys Glu
145             150             155             160
Cys Glu Glu Gln Phe Arg Gly Ser Val Gly Lys Asn Ile Glu Gln Leu
165             170             175
Glu Glu Arg Val Lys Asp Ser Leu Ala Ile Ile Lys Arg Ile Asn Asn
180             185             190
Leu Gly Leu Asn Pro Asn Ser Asn Phe Asn Met Asp Ser Gly Ile Asp
195             200             205
Thr Ile Gly Leu Phe Ser Ser Ile Gly Gly Leu Val Leu Leu Leu Leu
210             215             220
Thr Pro Val Val Gly Glu Phe Ala Leu Ile Ala Gly Val Gly Leu Ala
225             230             235             240
Leu Val Gly Val Gly Lys Ser Ile Trp Ser Phe Phe Asp Ser Asp Tyr
245             250             255

```

SUBSTITUTE SHEET (RULE 26)

1281

```

Lys Lys Ser Gln Gln Arg Lys Glu Val Asp Lys Asn Leu His Gln Ile
      260      265      270
Cys Glu Lys Ile Val Gln Asp Val Lys Ser Arg Ile Glu Ser Tyr Lys
      275      280      285
Asn Gly Ala Leu Gly Met Ile Glu Glu Leu Asn Ala Gly Phe Asn Lys
      290      295      300
Leu Val Asp His Tyr Glu Arg Met Lys Arg Gln Leu Glu Glu Ala His
      305      310      315      320
Glu Lys Leu Gly Tyr Ile Tyr Asn Ser Ile His Leu Thr Ile Ser Asn
      325      330      335
Arg Arg Ile Gln
      340

```

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744

```

Ser Ala Leu Trp His Lys Asp Pro Thr Thr Ile Lys Gln Phe Gly Leu
1      5      10      15
Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu Leu Leu Ile Val
      20      25      30
Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys Tyr
      35      40      45
Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala Ile
      50      55      60
Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly Thr
      65      70      75      80
Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln Gln
      85      90      95
Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro Leu
      100      105      110
Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met His
      115      120      125
Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu Gly
      130      135      140
Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe Met
      145      150      155      160
Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly Asp
      165      170      175
Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn Ala
      180      185      190
Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly Asp Val Ile Trp
      195      200      205
Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
      210      215

```

(2) INFORMATION FOR SEQ ID NO:1745:

SUBSTITUTE SHEET (RULE 26)

1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745

```

Gly Ile Lys Leu Gly Gly Ile Asn Met Ala Gly Thr Gln Ala Ile Tyr
1           5           10           15
Glu Ser Ser Ser Ala Gly Phe Leu Ser Gln Val Ser Ser Ile Ile Ser
20           25           30
Ser Thr Ser Gly Val Ala Gly Pro Phe Ala Gly Ile Val Ala Gly Ala
35           40           45
Met Thr Ala Ala Ile Ile Pro Ile Val Val Gly Phe Thr Asn Pro Gln
50           55           60
Met Thr Ala Ile Met Thr Gln Tyr Asn Gln Ser Ile Ala Glu Ala Val
65           70           75           80
Ser Val Pro Met Lys Ala Ala Asn Gln Gln Tyr Ser Gln Leu Tyr Gln
85           90           95
Gly Phe Asn Asp Gln Ser Met Ala Val Gly Thr Ile Ser
100           105

```

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746

```

Phe Gln Phe Glu Arg Lys Arg Met Lys Phe Phe Thr Arg Ile Thr Asp
1           5           10           15
Ser Tyr Lys Lys Val Val Val Thr Leu Gly Leu Val Val Thr Thr Asn
20           25           30
Pro Leu Met Ala Val Thr Ser Pro Ala Thr Gly Val Thr Glu Thr Lys
35           40           45
Ser Leu Val Ile Gln Ile Ile Ser Val Leu Ala Ile Val Gly Gly Cys
50           55           60
Ala Leu Gly Val Lys Gly Ile Ala Asp Ile Trp Lys Ile Ser Asp Asp
65           70           75           80

```

SUBSTITUTE SHEET (RULE 26)

1283

Ile Lys Arg Gly Gln Ala Thr Val Phe Ala Tyr Ala Gln Pro Ile Ala
 85 90 95
 Met Leu Ala Val Ala Gly Gly Ile Ile Tyr Leu Ser Thr Lys Phe Gly
 100 105 110
 Phe Asn Ile Gly Glu Ser Gly Gly Ala Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747

Ser Gly Ile Ser Ile Lys Arg Gly Val Phe Val Ala Ser Lys Gln Ala
 1 5 10 15
 Asp Glu Gln Lys Lys Leu Val Ile Glu Gln Glu Val Gln Lys Arg Gln
 20 25 30
 Phe Gln Lys Ile Glu Glu Leu Lys Ala Asp Met Gln Lys Gly Val Asn
 35 40 45
 Pro Phe Phe Lys Val Leu Phe Asp Gly Gly Asn Arg Leu Phe Gly Phe
 50 55 60
 Pro Glu Thr Phe Ile Tyr Ser Ser Ile Phe Ile Leu Phe Val Thr Ile
 65 70 75 80
 Val Leu Ser Val Ile Leu Phe Gln Ala Tyr Glu Pro Val Leu Ile Val
 85 90 95
 Ala Ile Val Ile Val Leu Val Ala Leu Gly Phe Lys Lys Asp Tyr Arg
 100 105 110
 Leu Tyr Gln Arg Met Glu Arg Ala Met Lys Phe Lys Lys Pro Phe Leu
 115 120 125
 Phe Lys Gly Val Lys Asn Lys Ala Phe Met Ser Ile Phe Ser Met Lys
 130 135 140
 Pro Ser Lys Glu Met Ala Asn Asp Ile His Leu Asn Pro Asn Arg Glu
 145 150 155 160
 Asp Arg Leu Val Ser Ala Ala Asn Ser Tyr Leu Ala Asn Asn Tyr Glu
 165 170 175
 Cys Phe Leu Asp Asp Gly Val Ile Leu Thr Asn Asn Tyr Ser Leu Leu
 180 185 190
 Gly Thr Ile Lys Leu Gly Gly Ile Asp Phe Leu Thr Thr Ser Lys Lys
 195 200 205
 Asp Leu Ile Glu Leu His Ala Ser Ile Tyr Ser Val Phe Arg Asn Phe
 210 215 220
 Val Thr Pro Glu Phe Lys Phe Tyr Phe His Thr Val Lys Lys Lys Ile
 225 230 235 240
 Val Ile Asp Glu Thr Asn Arg Asp Tyr Gly Leu Ile Phe Ser Asn Asp
 245 250 255
 Phe Met Arg Ala Tyr Asn Glu Lys Gln Lys Arg Glu Ser Phe Tyr Asp
 260 265 270
 Ile Ser Phe Tyr Leu Thr Ile Glu Gln Asp Leu Leu Asp Thr Leu Asn
 275 280 285
 Glu Pro Val Met Asn Lys Lys His Phe Ala Asp Asn Asn Phe Glu Glu

SUBSTITUTE SHEET (RULE 26)

1284

| | | | | |
|---|--|-----|--|-----|
| 290 | | 295 | | 300 |
| Phe Gln Arg Ile Ile Arg Ala Lys Leu Glu Asn Phe Lys Asp Arg Ile | | | | |
| 305 | | 310 | | 315 |
| Glu Leu Ile Glu Glu Leu Ser Lys Tyr His Pro Thr Arg Leu Lys | | | | 320 |
| | | 325 | | 330 |
| Glu Tyr Thr Lys Asp Gly Ile Ile Tyr Ser Lys Gln Cys Glu Phe Tyr | | | | 335 |
| | | 340 | | 345 |
| Asn Phe Leu Val Gly Met Asn Glu Ala Pro Phe Ile Cys Asn Arg Lys | | | | 350 |
| | | 355 | | 360 |
| Asp Leu Tyr Leu Lys Glu Lys Met His Gly Gly Val Lys Glu Val Tyr | | | | 365 |
| | | 370 | | 375 |
| Phe Ala Asn Lys His Gly Lys Ile Leu Asn Asp Leu Ser Glu Lys | | | | 380 |
| | | 385 | | 390 |
| Tyr Phe Ser Ala Ile Glu Ile Ser Glu Tyr Ala Pro Lys Ser Gln Ser | | | | 395 |
| | | 405 | | 410 |
| Asp Leu Phe Asp Lys Ile Asn Ala Leu Asp Ser Glu Phe Ile Phe Met | | | | 415 |
| | | 420 | | 425 |
| His Ala Tyr Ser Pro Lys Asn Ser Gln Val Leu Lys Asp Lys Leu Ala | | | | 430 |
| | | 435 | | 440 |
| Phe Thr Ser Arg Arg Ile Ile Ser Gly Gly Ser Lys Glu Gln Gly | | | | 445 |
| | | 450 | | 455 |
| Met Thr Leu Gly Cys Leu Ser Glu Leu Val Gly Asn Gly Asp Ile Thr | | | | 460 |
| | | 465 | | 470 |
| Leu Gly Ser Tyr Gly Asn Ser Leu Val Leu Phe Ala Asp Ser Phe Glu | | | | 475 |
| | | 485 | | 490 |
| Lys Met Lys Gln Ser Val Lys Glu Cys Val Ser Ser Leu Asn Ala Lys | | | | 495 |
| | | 500 | | 505 |
| Gly Phe Leu Ala Asn Ala Ala Thr Phe Ser Met Glu Asn Tyr Phe Phe | | | | 510 |
| | | 515 | | 520 |
| Ala Lys His Cys Ser Phe Ile Thr Leu Pro Phe Ile Phe Asp Val Thr | | | | 525 |
| | | 530 | | 535 |
| Ser Asn Asn Phe Ala Asp Phe Ile Ala Met Arg Ala Met Ser Phe Asp | | | | 540 |
| | | 545 | | 550 |
| Gly Lys Glu Asp Asn Asn Ala Trp Gly Asn Ser Val Met Thr Leu Lys | | | | 555 |
| | | 565 | | 570 |
| Ser Glu Ile Asn Ser Pro Phe Tyr Leu Asn Phe His Met Pro Thr Asp | | | | 575 |
| | | 580 | | 585 |
| Phe Gly Ser Ala Ser Ala Gly His Thr Leu Ile Leu Gly Ser Thr Gly | | | | 590 |
| | | 595 | | 600 |
| Ser Gly Lys Thr Val Phe Met Ser Met Thr Leu Asn Ala Met Gly Gln | | | | 605 |
| | | 610 | | 615 |
| Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys Asp Lys Gln Lys Leu | | | | 620 |
| | | 625 | | 630 |
| Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala Tyr Gly Asn Ile Val | | | | 635 |
| | | 645 | | 650 |
| Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu Gly Thr Asp Thr Gly | | | | 655 |
| | | 660 | | 665 |
| Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln Lys Thr Asn Ala Thr | | | | 670 |
| | | 675 | | 680 |
| Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val Lys Glu Leu Val Lys | | | | 685 |
| | | 690 | | 695 |
| Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu Asn Gly Asn Ser Ile | | | | 700 |
| | | 705 | | 710 |
| Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala Ala Val Thr Asn | | | | 715 |
| | | 725 | | 730 |
| Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro Ile Thr Gln Leu Ile | | | | 735 |
| | | 740 | | 745 |
| Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn Gly Leu Val Ala Arg | | | | 750 |
| | | 755 | | 760 |
| Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu Phe Gln Trp Leu Phe | | | | 765 |
| | | 770 | | 775 |
| Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser Lys Thr Ile Ile Gly | | | | 780 |
| | | 785 | | 790 |
| Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp Val Ser Pro Phe Ile | | | | 795 |
| | | 805 | | 810 |
| | | | | 815 |

SUBSTITUTE SHEET (RULE 26)

1285

Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala Met Asp Gly Arg Arg
 820 825 830
 Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr Leu Gly Asp Pro Lys
 835 840 845
 Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr Ala Arg Lys Arg Asn
 850 855 860
 Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr Asp Leu Leu Ala Cys
 865 870 875 880
 Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro Thr Lys Ile Phe Leu
 885 890 895
 Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln Arg Leu Ala Asn Val
 900 905 910
 Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly Leu Asp Arg Lys Ile
 915 920 925
 Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile Ala Ser Phe Asn Leu
 930 935 940
 Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu Ser Thr Asp Thr Val
 945 950 955 960
 Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn His Ser Ile Ile Asp
 965 970 975
 Lys Tyr Gln Ala Leu Arg Gln Met Tyr Gln Gln Ile Lys Glu Tyr
 980 985 990

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748

Phe Leu Val Ala Leu Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr
 1 5 10 15
 Met Thr Asn Glu Ala Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe
 20 25 30
 Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val
 35 40 45
 Asp Asn Val Val Ala Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp
 50 55 60
 Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu
 65 70 75 80
 Arg Glu Glu Phe Ala Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
 85 90 95
 Gln Tyr Phe Ser Ser Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys
 100 105 110
 Asp Asn Leu Ile Asp Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe
 115 120 125
 Gly Thr Gln Arg Tyr Gln Ile Phe Met Asn Trp Val Ser His Gln Asn
 130 135 140
 Asp Pro Ser Lys Ile Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn
 145 150 155 160
 Ile Ile Gln Pro Pro Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu

SUBSTITUTE SHEET (RULE 26)

1286

165 170 175
 Arg Ser Ala Lys Gln Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile
 180 185 190
 Arg Ser Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu
 195 200 205
 Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly
 210 215 220
 Gly Asp Trp Leu Asp Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln
 225 230 235 240
 Ser Ser Asp Leu Lys Glu Thr Leu Asn Gln Glu Pro Val Pro His Val
 245 250 255
 Gln Pro Asp Val Ala Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro
 260 265 270
 Glu Ala Arg Asp Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr
 275 280 285
 Leu Gly Asp Met Asn Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp
 290 295 300
 Pro Asn Tyr Lys Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser
 305 310 315 320
 Ser Val Leu Met Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser
 325 330 335
 Leu Leu Tyr Gly Asn Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn
 340 345 350
 Ala Thr Val Gly Tyr Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu
 355 360 365
 Ile Asn Val His Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly
 370 375 380
 Glu Lys Gly Ile Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln
 385 390 395 400
 Leu Thr Gly Ser Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys
 405 410 415
 Val Asp Phe Met Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn
 420 425 430
 Leu Ser Lys Lys Glu Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp Phe
 435 440 445
 Gln Lys Asp Ser Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile
 450 455 460
 Ala Phe Val Ser Lys Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu
 465 470 475 480
 Phe Gly Asn Gly Glu Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys
 485 490 495
 Ala Asp Lys Ala Leu Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser
 500 505 510
 Leu Lys His Asp Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr
 515 520 525
 Thr Asn Ala Ser Lys Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly
 530 535 540
 Val Ser His Leu Glu Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu
 545 550 555 560
 Pro Asn Leu Asn Asn Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu
 565 570 575
 Glu Asp Lys Leu Ile Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys
 580 585 590
 Leu Val Lys Asp Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala
 595 600 605
 Leu Asn Phe Asn Lys Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr
 610 615 620
 Asp Glu Val Lys Gln Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys
 625 630 635 640
 Arg Glu Arg Leu Glu Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser
 645 650 655
 Gly Asn Lys Asn Lys Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys
 660 665 670
 Asp Glu Ile Phe Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg
 675 680 685

SUBSTITUTE SHEET (RULE 26)

1287

Ala Ile Ala Tyr Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser
 690 695 700
 Asp Lys Leu Glu Asn Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser
 705 710 715 720
 Phe Asp Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu
 725 730 735
 Glu Thr Leu Lys Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn
 740 745 750
 Pro Glu Trp Ile Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu
 755 760 765
 Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys
 770 775 780
 Ser Asp Leu Glu Asn Ser Ile Lys Asp Val Ile Ile Asn Gln Lys Ile
 785 790 795 800
 Thr Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala
 805 810 815
 Thr Gly Asp Phe Ser Gly Val Glu Gln Ala Leu Ala Asp Leu Lys Asn
 820 825 830
 Phe Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe
 835 840 845
 Asn Thr Gly Lys Asn Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val
 850 855 860
 Asn Gly Thr Leu Val Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr
 865 870 875 880
 Leu Ser Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu
 885 890 895
 Gly Asn Phe Asn Asn Asn Asn Asn Gly Leu Glu Asn Ser Thr Glu
 900 905 910
 Pro Ile Tyr Thr Gln Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg
 915 920 925
 Leu Asp Gln Ile Ala Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser
 930 935 940
 Phe Leu Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly
 945 950 955 960
 Leu Ser Ala Asn His Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly
 965 970 975
 Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys
 980 985 990
 Val Gly Leu Ser Arg Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu
 995 1000 1005
 Asn Gln Ala Val Ser Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp
 1010 1015 1020
 Gln Met Ile Asp Lys Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn
 1025 1030 1035 1040
 Leu Tyr Val Glu Ser Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys
 1045 1050 1055
 Leu Asp Asn Tyr Ala Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val
 1060 1065 1070
 Lys Asn Gly Thr Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys
 1075 1080 1085
 Asn Ser Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn
 1090 1095 1100
 Val Gly Ser Ala Pro Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln
 1105 1110 1115 1120
 Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu
 1125 1130 1135
 Ser Asn Ala Val Lys Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr
 1140 1145 1150
 Asn Ile Phe Ser Met Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu
 1155 1160 1165
 His Gly Val Lys Asn Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:1749:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749

```

Ala Leu Ser Leu Ala Ser Ile Leu Ala Arg Val Glu Glu Leu Ala Lys
1      5      10      15
Leu Ile Asn Asn Asn Asn Asn Lys Lys Leu Arg Gly Phe Phe Leu
20      25      30
Lys Val Leu Leu Ser Leu Val Val Phe Ser Ser Tyr Gly Ser Ala Asn
35      40      45
Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu Glu Lys Glu Lys Asn Thr
50      55      60
Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp Phe Asp Ser Phe Lys Ala
65      70      75      80
Thr Ile Lys Asn Leu Lys Asp Lys Lys Val Thr Phe Lys Glu Val Asn
85      90      95
Pro Asp Ile Ile Lys Asp Glu Val Phe Asp Phe Val Ile Val Asn Arg
100     105     110
Val Leu Lys Lys Ile Lys Asp Leu Lys His Tyr Asp Pro Val Ile Glu
115     120     125
Lys Ile Phe Asp Glu Lys Gly Lys Glu Met Gly Leu Asn Val Glu Leu
130     135     140
Gln Ile Asn Pro Glu Val Lys Asp Phe Phe Thr Phe Lys Ser Ile Ser
145     150     155     160
Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser Leu His Gly Glu Thr Arg
165     170     175
Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn Val Leu Leu Ala Val Phe
180     185     190
Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys His Ile Ser Thr Ile Glu
195     200     205
Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr Cys Glu Ala Val Tyr Leu
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750

```

Asn Asn Ala Lys Asn Lys Asn Lys Gly Val Lys Ser Met Lys Thr Asn
1      5      10      15
Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu Ile Ile Gly Met
      20      25      30
Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp Ile Lys Asp Ile
      35      40      45
Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu Val Ser Arg Asp
      50      55      60
Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu Gln Lys Val Ala
65      70      75      80
Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile Lys Phe Asp Asp
      85      90      95
Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu Gly Ile Asn Ala
      100      105      110
Met Trp Gly Ile Gln Asn Leu Leu Met Ser Gln Met Met Ser Asn Tyr
      115      120      125
Gly Pro Asn Asn Ser Phe Met Tyr Gly Tyr Ala Pro Thr Tyr Ser Asp
130      135      140
Ser Ser Phe Leu Pro Pro Ile Leu Gly Tyr
145      150

```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751

```

Pro Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys
1      5      10      15
Pro Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met
      20      25      30
Ile Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp
      35      40      45
Ile Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln
      50      55      60
Tyr Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile
65      70      75      80
Lys Ile Ser Gln Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp
      85      90      95
Ala Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln
      100      105      110
Ile Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn
      115      120      125
Gln Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr
130      135      140
Lys Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys

```

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```

145          150          155          160
Asp Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser
165          170          175
His Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile
180          185          190
Leu Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu
195          200          205
Gln Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile
210          215          220
Leu Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu
225          230          235          240
Met Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr
245          250          255
Ser Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr
260          265          270
Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr
275          280          285
Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln
290          295          300
Val Lys His Asp Leu Asn Met Gln Lys Ala Asn Glu Lys Ala Leu Arg
305          310          315          320
Ser Tyr Ile Ala Leu Lys Lys Gly Asn Ala Gln Asn Tyr Thr Thr Gln
325          330          335
Asp Phe Glu Lys Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys
340          345          350
Leu Thr Ala Leu Lys Pro Leu Glu Val Leu Lys Pro Glu Pro Phe Lys
355          360          365
Asp Gly Phe Ile Val Val Gln Leu Val Ser Gln Ile Lys Asp Glu Leu
370          375          380
Gln Asn Phe Asp Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln
385          390          395          400
Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys
405          410          415
Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly
420          425          430
Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Thr
435          440          445
Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Val Thr Ile Gly Asn Lys
450          455          460
Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Pro Phe Ser
465          470          475          480
Ala Glu Glu Asn Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr
485          490          495
Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys
500          505          510
Ile Val Lys Tyr Ile Gln
515

```

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752

```

Lys Gly Lys Leu Gly Leu Phe Tyr Tyr Phe Ser Asp Leu Leu Glu Ser
1      5      10      15
Leu Ile Cys Phe Ser Asn Ser Cys Cys Lys Ala Cys Cys Cys Phe Ser
20      25      30
Phe Phe Glu Arg Arg Arg Phe Phe Leu Gly Phe Phe Ser Phe Phe Glu
35      40      45
Glu Val Ser Gly Ser Phe Glu Ala Val Ser Leu Ser Val Leu Ala Leu
50      55      60
Val Ile Gly Ser Arg Ser Gly Leu Glu Glu Phe Cys Val Leu Glu Glu
65      70      75      80
Leu Ile Asn Ser Gly Leu Ser Val Trp Leu Ser Ser Ser Pro Leu Leu
85      90      95
Leu Phe Trp Asn Ala Ala Leu Val Ser Phe Ser Ala Cys Ser Ser Ile
100     105     110
Phe Leu Arg Thr Ile Ala Ser Thr Phe Leu Ala Phe Ser Phe Trp Leu
115     120     125
Thr Leu Thr Met Leu Ile Lys Tyr Leu Ile Tyr Pro Ser Tyr Met Ser
130     135     140
Pro Asn Cys Ser Cys Lys Ala Pro Lys Ser Glu Pro Leu
145     150     155

```

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753

```

Gly Leu Leu Lys Pro Leu Glu Glu Thr Glu Ile Lys Ala Cys Asn Lys
1      5      10      15
Asp Ile Leu Pro Leu Lys Pro Tyr Glu Lys Ala Lys Leu Ile Ala Tyr
20      25      30
Ile Pro Gln Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe
35      40      45
Val Leu Met Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys
50      55      60
Ala Lys His Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu
65      70      75      80
Glu Ser Leu Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg
85      90      95
Gln Met Val Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu
100     105     110
Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu
115     120     125
Phe Phe Asp Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val
130     135     140
Leu Val Asn Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His

```

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```

145          150          155          160
Val Val Met Leu Lys Asp Lys Lys Leu Phe Leu Gln Ala Ser Thr Pro
          165          170          175
Ile Ala Met Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu
          180          185          190
Glu Ala Ile Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
          195          200          205

```

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754

```

Lys Lys Lys Lys Asn Asp Glu Lys His Ile Ala Lys His Phe Val Ala
1      5      10      15
Val Ser Thr Asn Lys Glu Ala Val Gln Gln Phe Gly Ile Asp Glu His
20     25     30
Asn Met Phe Gly Phe Trp Asp Phe Val Gly Gly Arg Tyr Ser Leu Trp
35     40     45
Ser Ala Ile Gly Leu Ser Ile Met Ile Tyr Leu Gly Lys Lys Asn Phe
50     55     60
Asn Ala Leu Leu Lys Gly Ala Tyr Leu Met Asp Glu His Phe Arg Asn
65     70     75     80
Ala Pro Phe Glu Ser Asn Leu Pro Val Leu Met Gly Leu Ile Gly Val
85     90     95
Trp Tyr Ile Asn Phe Phe Gln Ser Lys Gly His Leu Ile Ala Pro Tyr
100    105    110
Asp

```

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755

```

His Asn Lys Thr Arg Met Lys Arg Ala Lys Arg Arg Lys Phe Ile Thr
1      5      10      15
Lys Phe Ser Arg Tyr Tyr Thr Pro Ser Val Leu Phe Ile Ala Leu Met
      20      25      30
Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu Trp
      35      40      45
Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala Leu
      50      55      60
Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala Ser
      65      70      75      80
Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Val Leu Thr
      85      90      95
Gln Thr Lys Ser Ile Ala Phe Asp Lys Thr Gly Thr Leu Thr Lys Gly
      100      105      110
Val Phe Lys Val Val Asp Ile Val Pro Gln Asn Gly His Ser Lys Glu
      115      120      125
Glu Val Cys Ile Thr Leu Leu Ala Arg Ser Phe Tyr Pro Arg Thr Arg
      130      135      140
Ser Leu Tyr Pro Phe Lys Lys His Ala Lys Lys Cys
      145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756

```

Arg Ser Thr Leu Ala Ser Ala Asp Val Gly Ile Gly Met Gly Lys Gly
1      5      10      15
Ser Glu Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser
      20      25      30
Leu Ser Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser
      35      40      45
Ile Ile Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe
      50      55      60
Ile Val Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe
      65      70      75      80
Gly Asp Val Gly Val Thr Leu Leu Asp Leu Ala Asn Ser Met Arg Thr
      85      90      95
Met Arg Ala

```

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757

```

His Gln Ser Phe Lys Arg Ala Phe Glu Pro Arg Arg Lys Gly Arg Val
1      5      10      15
Phe Arg Ile Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly
20      25      30
Ala Gln Lys Ile Ala Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu
35      40      45
Ala Gly Ala Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala
50      55      60
Tyr Leu Ile Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu
65      70      75      80
Thr Phe Thr Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys
85      90      95
Leu Leu Lys Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His
100     105     110
Arg Phe Gly Leu Leu Phe Leu Arg Gln His Met Asn Leu Lys Arg
115     120     125
Ala Cys Asp Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys
130     135     140
Lys Gln Leu Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys
145     150     155     160
Asn Gly Met Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala
165     170     175
Tyr Glu Leu Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Asp Phe
180     185     190
Asp Asp Leu Leu Cys Leu Ser Leu Lys Ile Leu Gln Asp Asn Glu Lys
195     200     205
Leu Ala Lys Glu Thr Ser Glu Arg Tyr His Tyr Ile Met Val Asp Glu
210     215     220
Tyr Gln Asp Thr Asn Ala Leu Gln Leu Glu Phe Leu Lys Gln Leu Ser
225     230     235     240
Phe Thr His His Asn Leu Cys Val Val Gly Asp Asp Asp Gln Ser Ile
245     250     255
Tyr Gly Phe Arg Gly Ala Asp Ile Ser Asn Ile Leu Asn Phe Ser Lys
260     265     270
His Phe Lys Gly Ala Lys Ile Val Lys Leu Glu Thr Asn Tyr Arg Ser
275     280     285
Ser Ala Glu Ile Leu Ala Cys Ala Asn Ser Leu Ile Ser His Asn Gln
290     295     300
His Arg His Ile Lys Thr Leu Gln Ser Phe Lys Gly Ser His Lys Ser
305     310     315     320
Val Ile Cys Lys Glu Tyr Pro Thr Gln Lys Glu Glu Ser Leu Asp Val
325     330     335
Ala Tyr Gln Ile Gln Ser Pro Phe Lys Glu Gly Arg Glu Phe Arg Lys
340     345     350
Tyr Arg Tyr Phe Val Ser Phe Lys Trp
355     360

```

(2) INFORMATION FOR SEQ ID NO:1758:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758

```

Phe Val Leu Asn Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu
1      5      10      15
Asn Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile
20      25      30
Pro Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser
35      40      45
Ser Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr
50      55      60
Ile Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu
65      70      75      80
Ser Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln
85      90      95
Thr Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn
100     105     110
Ala Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile
115     120     125
Gly Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met
130     135     140
Met Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala
145     150     155     160
Leu His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser
165     170     175
His Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala
180     185     190
Leu Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val
195     200     205
Ser Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp
210     215     220
Leu Tyr Tyr His Tyr Leu Lys Ile Val Arg Asp Thr Leu Tyr Lys Asp
225     230     235     240
Tyr Lys Lys Ser Phe Tyr Ser Tyr Ala Tyr Ala Leu Lys Ser Tyr Tyr
245     250     255
Ala Gly Glu Tyr Phe Glu Ala Leu Ser Pro Leu Met His Pro Asn Ser
260     265     270
Asn Ala Phe Leu Lys Pro Asn Ala Arg Leu Ala Ser Lys Leu Phe Leu
275     280     285
Met Phe Lys Asp Glu Thr Asn Ala Tyr Lys Gln Leu Gln Lys Ser Ala
290     295     300
Asn Ala Gln Asp Glu Leu Ala Leu Gly Leu Leu Gln Ala Arg Leu Gly
305     310     315     320
Thr Tyr Lys Gln Ala Leu Glu His Leu Gln His Tyr Leu His Asn Tyr
325     330     335
Pro Lys Asp Leu Asn Ala Leu Met Ala Leu Glu Leu Val Ser Leu Lys
340     345     350
Met Gly Asp Thr Leu Lys Ala Ser Glu Ala Leu Lys Leu Ala Ser His
355     360     365
Thr Gln Glu Asp Thr Leu Leu Ala Asn Ser Phe Tyr Pro Ile Lys Pro

```

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| | | |
|-----------------------------|-------------------------|-----------------|
| 370 | 375 | 380 |
| Thr Ile Asn Pro Met Phe | Leu Asp Lys Glu Arg Ala | Lys Glu Arg Phe |
| 385 | 390 | 395 |
| Trp Asn Thr Gln Tyr Phe | Glu Gly Lys Arg Asp Phe | Ile Tyr Arg Leu |
| 405 | 410 | 415 |
| Leu Phe Tyr Tyr Ala Pro Phe | Lys Val Leu Asp Ser Lys | Glu Thr Leu |
| 420 | 425 | 430 |
| Gly Val Ile Glu Glu Gly Leu | Phe Leu Leu Asp Ser Asp | Thr Gln Lys |
| 435 | 440 | 445 |
| Asp Leu Glu Gly Ala Ser Leu | Ala Phe Lys Arg Gly Arg | Leu Met Ala |
| 450 | 455 | 460 |
| Ile Ala Asp Lys Asn Ala Leu | Lys Gly Leu Lys Glu Leu | Glu Lys Lys |
| 465 | 470 | 475 |
| Arg Leu Lys Lys Ala Leu Ser | Phe Phe Asp Leu Ser Leu | Lys Asn Ser |
| 485 | 490 | 495 |
| Pro Asn Asn Ala Leu Leu His | Tyr Asn Val Gly Leu Ile | Tyr Ala Gln |
| 500 | 505 | 510 |
| Leu Glu Asn Tyr His Lys Ala | Tyr Phe His Phe Leu Arg | Ala Phe His |
| 515 | 520 | 525 |
| Leu Asn Ser Ala Asp Tyr Leu | Ser Ala Val Phe Ala Val | Leu Ala Ser |
| 530 | 535 | 540 |
| His Phe Thr His Glu Asp Thr | Thr Glu Phe Leu Arg Glu | Ile Thr Glu |
| 545 | 550 | 555 |
| Asn Phe Tyr Ser His Asp Phe | Ser Ser Pro Thr Gln Lys | Ala Leu Leu |
| 565 | 570 | 575 |
| Ser Ser Leu Ile Ala Tyr Leu | Asn Tyr Arg Thr Asn Trp | Asp Met Asp |
| 580 | 585 | 590 |
| Trp Leu Lys Asn Ala Pro Lys | Lys Leu Pro Phe Tyr Tyr | Ala Leu Glu |
| 595 | 600 | 605 |
| Ala Val Phe Ala Lys Glu Ser | Lys Asp Lys Lys Leu Met | Val Gln Ser |
| 610 | 615 | 620 |
| Phe Gly Asn Leu Lys Lys Met | Leu Pro Lys Asp Leu Ile | Ser Asn Ile |
| 625 | 630 | 635 |
| Phe Tyr Glu Ile Val Ser Tyr | Tyr Asp Ala Ser Ile Arg | His Thr Leu |
| 645 | 650 | 655 |
| Ser Ile Tyr Thr Leu Leu Asp | Ser His Lys Ile Ser Trp | Asp Gln Thr |
| 660 | 665 | 670 |
| Met Gln Gly Pro Ile Leu Gly | Arg His Phe Tyr Thr Tyr | Met Gly Phe |
| 675 | 680 | 685 |
| Met Val Asn Asp Leu Asp His | Gln Glu Arg Leu Leu Glu | Gln Lys Ile |
| 690 | 695 | 700 |
| Ala Ser Leu Glu Arg Gly Glu | Ala Pro Asn Asp Trp Leu | Glu Asn Leu |
| 705 | 710 | 715 |
| Ala Leu Val Ser Leu Phe Gln | Gly Gln Tyr Glu Lys Ala | Ser Ala Leu |
| 725 | 730 | 735 |
| Tyr Gln Asn Leu Ile Asp Gly | Leu Lys Asp Asn Glu Ala | Arg Leu Lys |
| 740 | 745 | 750 |
| Ile Leu Ala Gly Leu Thr Tyr | Ile Ala Gln Asn Asn Tyr | Asn Asn Ala |
| 755 | 760 | 765 |
| Ala Leu Trp Leu Glu Leu Gly | Lys Leu Asp Asp Pro Asn | Asn Glu Asn |
| 770 | 775 | 780 |
| Ile Arg Tyr Ala Leu Gly Leu | Leu Tyr Gln Arg Lys Gly | Asp Leu Lys |
| 785 | 790 | 795 |
| Ser Ala Leu Asn His Phe Leu | Ala Ile Lys Thr Ser Asp | Phe Ser Ser |
| 805 | 810 | 815 |
| Pro Tyr Phe Asp Phe Glu Ile | Asp Thr Asn Leu Leu Lys | Glu Arg Leu |
| 820 | 825 | 830 |
| Asn Gln Glu Glu Lys Gly Glu | Phe Leu Glu | |
| 835 | 840 | |

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759

```

Lys Val Thr Thr Thr Met Ile Lys Ala Ile Ile Gly Lys Ile Ile Gly
1      5      10      15
Thr Arg Asn Asp Arg Trp Ile Lys Gln Tyr Lys Lys Lys Val Leu Ala
20      25      30
Ile Asn Ala Leu Glu Pro Thr Tyr Glu Lys Met Ser Asp Val Glu Leu
35      40      45
Gln Asn Ala Phe Glu Glu Leu Lys Lys Arg Val Arg Ser Val Glu Lys
50      55      60
Asp Leu Gln Glu Lys Thr Leu Leu Glu Val Leu Pro Glu Ser Phe Ala
65      70      75      80
Ile Thr Arg Glu Ala Ser Lys Arg Ile Leu Lys Met Arg His Phe Asp
85      90      95
Val Gln Leu Ile Gly Gly Met Val Leu Asn Asp Gly Lys Ile Ala Glu
100     105     110
Met Lys Thr Gly Glu Gly Lys Thr Leu Val Ala Thr Leu Ala Val Ala
115     120     125
Leu Asn Ala Met Lys Gly Glu Ser Val Tyr Val Val Thr Val Asn Asp
130     135     140
Tyr Leu Ala His Arg Asp Ser Lys Glu Met Glu Pro Leu Tyr Gln Phe
145     150     155     160
Leu Gly Tyr Ser Val Gly Thr Ile Thr Ala Ser Val Arg Asp Asp Asp
165     170     175
Glu Arg Leu Glu Ile Tyr Ser Lys Asp Ile Val Tyr Gly Thr Asn Asn
180     185     190
Glu Phe Gly Phe Asp Tyr Leu Arg Asp Asn Met Lys Tyr Ser Leu Glu
195     200     205
His Lys Val Gln Lys Ser His Ala Phe Ala Ile Val Asp Glu Val Asp
210     215     220
Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Pro
225     230     235     240
Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val Ala Lys
245     250     255
Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn Arg Ala
260     265     270
Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu Phe Gly
275     280     285
Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His His Leu
290     295     300
Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys Asp Tyr
305     310     315     320
Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Glu Phe Thr Gly Arg
325     330     335
Leu Ser Glu Gly Arg Arg Phe Ser Glu Gly Leu His Gln Ala Leu Glu
340     345     350
Ala Lys Glu Ala
355

```

(2) INFORMATION FOR SEQ ID NO:1760:

SUBSTITUTE SHEET (RULE 26)

1298

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760

```

Lys Leu Phe Leu Lys Pro Leu Lys Glu Thr Ser Leu Ala Leu Val Gly
1      5      10      15
Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala Gly Leu Lys Arg
20      25      30
Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Phe Leu Ile Lys Arg Tyr
35      40      45
Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile Thr Ala Leu Leu
50      55      60
Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu Ile Val Ala Met
65      70      75      80
Ala Ile Met Asn Gly Met Ser Lys Glu Phe Glu Lys Lys Leu Phe Val
85      90      95
Met Asn Tyr Pro Leu Thr Leu Tyr Thr Thr Ser Pro Tyr Gly Ile Ser
100      105      110
Glu Glu Val Val Gln Ala Leu Glu Lys Lys Phe Pro Asn Leu Leu Phe
115      120      125
Ser Pro Tyr Leu Gln Thr Gln Ser Pro Ile Lys Ser Ala His Ser Met
130      135      140
Asn Gly Gly Val Val Phe Gly Val Asp Phe Ser Lys Glu Arg His Ile
145      150      155      160
Asn Glu Val Leu Asn Asp Ala Leu Lys Asn Ile Asn Glu Asn Asp Leu
165      170      175
Phe Lys Asn Pro Phe Asn Leu Ile Val Gly Lys Ser Leu Arg Tyr Ser
180      185      190
Leu Asn Leu Asp Leu Asn Gln Lys Ala Asp Leu Phe Phe Thr Glu Leu
195      200      205
Glu Pro Thr Gly Leu Thr Leu Ser Pro Ile Met Lys Arg Phe Thr Ile
210      215      220
Lys Gly Asp Phe Asp Ser Gly Leu Lys Ser Tyr Asp Met Ser Tyr Met
225      230      235      240
Tyr Ala Ser Leu Gln Ala Ile Ser Ala Ile Arg Arg Leu Pro Leu Gly
245      250      255
Leu Tyr Asp Gly Val His Val Tyr Ser Lys Thr Pro Met Lys Asp Ile
260      265      270
Glu Lys Leu Arg Asn Ala Leu Lys Thr Ile Asn His His Gly Ile Gly
275      280      285
Ile Glu Gly Trp Trp Gln Gln Asn Gly Asn Phe Phe Ser Ala Met Glu
290      295      300
Leu Glu Lys Arg Ala Leu Phe Ile Val Leu Met Leu Ile Ile Leu Met
305      310      315      320
Ala Ser Leu Asn Ile Ile Ser Ser Leu Leu Met Val Val Met Asn Arg
325      330      335
Arg Lys Glu Ile Ala Leu Leu Phe Ser Met Gly Ser Ser Gln Lys Glu
340      345      350
Ile Gln Lys Thr Phe Phe Tyr Leu Gly Asn Ile Ile Ser
355      360      365

```

SUBSTITUTE SHEET (RULE 26)

1299

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761

```

Arg Gly Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr
1      5      10      15
Phe Gln Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly
      20      25      30
Thr Ala Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu
      35      40      45
Val Val Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn
50      55      60
Asp Leu Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu
65      70      75      80
Lys Ile Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr
      85      90      95
Ala Ser Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu
      100     105     110
Arg Ile Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala
      115     120     125
Glu Ile Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr
      130     135     140
Asn Met Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys
145     150     155     160
Glu Leu Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg
      165     170     175
Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro
      180     185     190
Gly Val Ser Gln Phe Tyr Leu Ser Leu Glu Asp Asn Leu Leu Arg Ile
      195     200     205
Phe Gly Ser Asp Arg Thr Lys Gly Val Met Glu Lys Leu Gly Pro Lys
      210     215     220
Asp Gly Glu His Ile Glu Phe Lys Leu Val Thr Arg Ala Val Glu Asn
225     230     235     240
Ala Gln Lys Lys Val Glu Asn Leu His Phe Asp Ser Arg Lys His Leu
      245     250     255
Leu Glu Tyr Asp Asp Val Ala Asn Glu Gln Arg Thr Ser Val Tyr Asn
      260     265     270
Leu Arg Asp Glu Leu Leu Asp Ile Asn Tyr Asp Ile Ser Ala Lys Ile
      275     280     285
Ala Glu Asn Arg Glu Tyr Ala Leu Asn Gln Ile Phe Ser Lys Leu Lys
      290     295     300
Ala Phe Asp His Gln Asn Leu Ser Glu Glu Glu Leu Leu Gly Leu Lys
305     310     315     320
Asn Ile Leu Lys Glu Asp Phe Asn Ala Ser Val Glu Leu Glu Asp Leu
      325     330     335
Glu Lys Ala Ser Pro Ile Glu Ile Phe Val Ala Glu Lys Leu Lys Ser

```

SUBSTITUTE SHEET (RULE 26)

1300

Gly Leu 340 345 350

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762

```

Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1          5          10          15
Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
20          25          30
Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
35          40          45
Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
50          55          60
Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65          70          75          80
Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
85          90          95
Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser
100          105

```

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763

```

Lys Asn Gln Ile Leu Gln Ile Pro Leu Leu Pro Pro Pro Pro Asn Asn
1          5          10          15
Glu Glu Leu Leu Lys Ser Ile Thr Asp Leu Lys Asp Arg Leu Lys Lys
20          25          30

```

SUBSTITUTE SHEET (RULE 26)

1301

Leu Glu Asp Leu Lys Leu Glu Asp Phe Glu Pro Leu Arg Lys Leu Ser
 35 40 45
 His Phe Ile Val Ile Gly Asn Leu Phe Gly Lys Ser Ser Asn Asp Thr
 50 55 60
 Gln Glu Asn Pro Lys Asp Ala Leu Lys Ser Thr Asn Phe His Glu Lys
 65 70 75 80
 His Thr Lys Pro Thr Glu Thr Thr Glu Leu Val Glu Glu Asn Lys Ala
 85 90 95
 Leu Thr Thr Glu Lys Glu Arg Leu Glu Arg Glu Asn Lys Asn Leu Thr
 100 105 110
 Ala Asp Lys Glu Asn Leu Thr Lys Glu Lys Thr Glu Leu Gln Lys Gln
 115 120 125
 Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Glu Asn Glu Lys Ala
 130 135 140
 Asp Trp Leu Arg Glu Lys Glu Asn Leu Thr Lys Asp Arg Glu Asn Leu
 145 150 155 160
 Thr Lys Glu Lys Thr Glu Leu Thr Glu Lys Asn Lys Val Leu Thr Thr
 165 170 175
 Glu Lys Glu Arg Leu Ala Thr Glu Lys Glu Asn Leu Thr Lys Glu Lys
 180 185 190
 Thr Glu Ser Gln Lys Gln Val Asn Glu Leu Lys Asn Ser Lys Gln Val
 195 200 205
 Leu Glu Asn Glu Lys Ala Asp Leu Thr Asn Glu Asn Thr Lys Leu Lys
 210 215 220
 Thr Asp Lys Thr Asp Leu Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu
 225 230 235 240
 Lys Thr Glu Leu Asn Asn Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu
 245 250 255
 Arg Leu Ala Ala Asp Lys Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg
 260 265 270
 Lys Pro Asn
 275

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764

Ala Leu Ser Asn Cys Leu Ser Leu Ser Val Arg Arg Trp Phe Ser Phe
 1 5 10 15
 Ser Lys Leu Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn
 20 25 30
 Arg Ala Arg Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val
 35 40 45
 Thr Trp Trp Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser
 50 55 60
 Leu Val Ser Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe
 65 70 75 80
 Ser Leu Ser Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg

SUBSTITUTE SHEET (RULE 26)

1302

```

      85          90          95
Ser Leu Ala Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe
      100          105          110
Ser Val Phe Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Phe Cys
      115          120          125
His Asn
      130

```

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1      5      10      15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
      20      25      30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
      35      40      45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
      50      55      60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
      65      70      75      80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
      85      90      95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
      100      105      110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
      115      120      125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
      130      135      140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
      145      150      155      160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
      165      170      175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180      185      190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
      195      200      205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
      210      215      220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
      225      230      235      240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Lys Ile Ala Ile Glu
      245      250      255
Lys Ser Glu Leu Glu Arg Glu Ile Ala Arg Leu Lys Ser Leu Glu Gly
      260      265      270
Met Glu Ala Lys Ser Asp Leu Asp Leu His Asn Arg Arg Leu Ala Ser
      275      280      285

```

SUBSTITUTE SHEET (RULE 26)

1303

Ala Asn Glu Asp Leu Lys Arg Gln Asn Arg Lys Leu Glu Glu Glu Asn
 290 295 300
 Ile Ala Leu Lys Glu Arg Val Asp Gly Leu Asn Glu Gln Leu Ser Lys
 305 310 315 320
 Leu Gln Pro Gln Lys Pro Gln
 325

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766

Phe Lys Thr Ile Glu Arg Asn Asp Phe Lys Leu Asn Gly Leu Thr Lys
 1 5 10 15
 Ile Leu Gln Asn Lys Gly Tyr Lys Met Lys Thr Ile Lys Asn Gly Ile
 20 25 30
 Met Ile Gly Thr Leu Gly Ala Leu Leu Ser Gly Cys Ser Ser Phe
 35 40 45
 Asp Ala Gln Arg Phe Ala Cys Leu Pro Lys Asp His Ser Ser Lys Asp
 50 55 60
 Ala Ser Thr Lys Lys Glu Ala Gln Tyr Ile Pro Lys Gly Phe Phe Asp
 65 70 75 80
 Pro Tyr Ser Ser Asn Leu Asn His Trp Asp Ser Thr Phe
 85 90

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767

Ser Leu Asn Lys Gly Leu Ala Leu Phe Leu Val Lys Lys Ile Gly Val
 1 5 10 15
 Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser Phe

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```

      20      25      30
Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser Lys
      35      40      45
Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr Ile
      50      55      60
Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala Phe
      65      70      75      80
Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn Ser
      85      90      95
Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu Leu
      100      105      110
Ser Tyr Pro Asn Asp Pro Asn Asn Glu Asp Asn Ala Asn Asn Ser
      115      120      125
Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn Pro
      130      135      140
Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn Gly
      145      150      155      160
Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile Gln
      165      170      175
Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp Arg
      180      185      190
Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala Gln
      195      200      205
Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly Ser
      210      215      220
Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys Ser
      225      230      235      240
Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu Ile
      245      250      255
Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu Asp
      260      265      270
Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu Arg
      275      280      285
Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768

```

Ala Trp Leu Lys Ser Arg Val Leu Met Lys Arg Leu Ala Val Ala Leu
1      5      10      15
Ile Leu Val Leu Gly Val Val Trp Gly Lys Ser Leu Pro Lys Trp Ala
      20      25      30
Lys Asp Cys Ser Lys Glu Met Arg Ile Glu Lys Thr Gln Thr Lys Asp
      35      40      45
Glu Lys Ile Leu Val Cys Gly Met Ser Asp Ile Leu Leu Ser Asp Met
      50      55      60

```

1305

Asp Tyr Ser Leu Ser Ser Ala Arg Gln Asn Ala Leu Glu Lys Val Met
 65 70 75 80
 Glu Ala Phe Lys Gly Asp Arg Ile Glu Ile Lys Ala Gly Glu Leu Lys
 85 90 95
 Ala Thr Phe Ile Asp Thr Asp Lys Val Tyr Val Leu Leu Arg Ile Thr
 100 105 110
 Lys Lys His Val Ala Leu Met Asn Glu
 115 120

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769

Gly Leu Ile Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val
 1 5 10 15
 Gly Ala Asn Leu Ser Ala Glu Pro Lys Lys Trp Tyr Ser Lys Ala Tyr Asn
 20 25 30
 Lys Thr Asn Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr
 35 40 45
 Ser Lys Glu Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser
 50 55 60
 Ile Ser Val Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val
 65 70 75 80
 Asp Asn Lys Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr
 85 90 95
 Asp Asp Leu Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln
 100 105 110
 Lys Gly Ile Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu
 115 120 125
 Gln Gly Leu Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr
 130 135 140
 Leu Met Pro Lys Val Cys Lys Gly Val Phe Tyr Lys Gln Ser Lys Ser
 145 150 155 160
 Met Gly Asp Leu Leu Ala Lys Ala Ala Pro Met Glu Arg Ile Leu Lys
 165 170 175
 Ala Tyr Ser Val Pro Val Ser Ser Leu Glu Asn Tyr Glu Lys Ile Tyr
 180 185 190
 Tyr Gln Asn Ala Phe Lys Pro Lys Val Arg Ile Ala Phe Asp Asp Asn
 195 200 205
 Ser Asp Thr Glu Ile Lys Asn Ala Leu Met Ser Ala Tyr Ala Arg Val
 210 215 220
 Leu Thr Pro Ser Asp Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val
 225 230 235 240
 Phe Thr Asp Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Ile Ile Ser
 245 250 255
 Ala Ser Asp Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val
 260 265 270
 Asp Glu Lys Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu

SUBSTITUTE SHEET (RULE 26)

1306

275. 280 285
 Tyr Lys Glu Leu Lys Gly Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr
 290 295 300
 Gly Leu
 305

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770

Pro Gln Arg Val Val Phe Arg Val Arg Phe Leu Leu Ala Ile Pro Gln
 1 5 10 15
 Ile Leu Val Gly Leu Arg Ile Ala Val Val Met Leu Val Ala Met Ala
 20 25 30
 Gly Ile Gly Ala Leu Ile Gly Ala Gly Gly Leu Gly Gln Ala Ile Phe
 35 40 45
 Arg Gly Leu Asn Thr Gln Asn Thr Thr Ile Leu Val Ala Gly Ser Phe
 50 55 60
 Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln Phe Val Ser Val Phe
 65 70 75 80
 Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser Gln Asn Ala Thr Gln
 85 90 95
 Lys Gln Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu
 100 105 110
 Leu Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Glu
 115 120 125
 Lys Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu
 130 135 140
 Gly Glu Ile Leu Ser Leu Leu Leu Glu Lys His His Ile Pro Ile Lys
 145 150 155 160
 Arg Ala Phe Gly Ile Gly Gly Gly Thr Met Asn Ile His Pro Ala Leu
 165 170 175
 Ile Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp
 180 185 190
 Val Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr
 195 200 205
 Ile Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu
 210 215 220
 Leu Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala
 225 230 235 240
 Gln Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro
 245 250 255
 Asn Phe Asp Phe Gly Ala Glu Phe Asp Phe Phe Glu Arg Glu Asp Ala
 260 265 270
 Phe Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His
 275 280 285
 Glu Met Asp Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser His Lys Ile
 290 295 300

SUBSTITUTE SHEET (RULE 26)

1307

Asn Ala Leu Asp Val Phe Thr Thr Asp Ala Gln Ile Lys Glu Leu Asp
 305 310 315 320
 Leu Lys Val Leu Lys Asp Asp Lys Gly Phe Phe Pro Asn Tyr Gln Ala
 325 330 335
 Gly Ile Val

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771

Gly Ala Lys Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser
 1 5 10 15
 Leu Gly Phe Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp
 20 25 30
 Ile Phe Tyr Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His
 35 40 45
 Thr Lys Gly Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala
 50 55 60
 Arg Glu Asp Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala
 65 70 75 80
 Ser Val Arg Tyr Ser Leu Gly Gly Val Ala Met Asp Asp Lys Ser Lys
 85 90 95
 Val Arg Gly Met Ala Leu Lys Leu Glu Asn Gln Asn Ala Ser Trp Thr
 100 105 110
 Met Val Met Leu Asn Thr Glu Ile Asn Phe Ala Lys Asn Pro Glu Glu
 115 120 125
 Phe Ala Gln Phe Phe Glu Met Arg Leu Pro Lys Asn Gly Gln Gly Arg
 130 135 140

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...528

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Glu | Phe | Leu | Ala | Ile | Asn | Glu | Leu | Met | Phe | Asp | Val | Phe | Leu | Pro | 1 | 5 | 10 | 15 |
| Ser | Arg | Leu | Lys | Gln | Lys | Glu | Leu | Leu | Glu | Lys | Ile | Glu | Val | Ile | Gln | 20 | 25 | 30 | |
| Lys | Phe | Phe | Pro | Asn | Phe | Pro | Lys | Glu | Thr | Leu | Leu | Asn | Asn | Tyr | Gln | 35 | 40 | 45 | |
| Lys | Glu | Asn | Ser | Leu | Tyr | Asn | His | Asn | Leu | Ile | Lys | Val | Val | Gly | Phe | 50 | 55 | 60 | |
| Ile | Pro | Tyr | Ala | Thr | Met | Gln | Ser | Leu | Tyr | Thr | Lys | Leu | Ile | Gln | Thr | 65 | 70 | 75 | 80 |
| Gln | Gly | Ile | Phe | Val | Arg | Pro | Leu | Asp | Lys | Arg | Tyr | Tyr | Pro | Asn | Asn | 85 | 90 | 95 | |
| Ala | Leu | Ala | Ser | His | Val | Leu | Gly | Tyr | Val | Gly | Val | Ala | Ser | Leu | Gln | 100 | 105 | 110 | |
| Asp | Leu | Lys | Asp | Asp | Glu | Glu | Asn | Gln | Tyr | Ser | Gln | Ile | Val | Gly | Lys | 115 | 120 | 125 | |
| Thr | Gly | Ile | Glu | Lys | Glu | Tyr | Asn | Lys | Phe | Leu | Gln | Gly | Lys | Val | Gly | 130 | 135 | 140 | |
| Tyr | Lys | Ile | Ile | His | Val | Asn | Ala | Leu | Asn | Gln | Glu | Leu | Ala | Thr | Leu | 145 | 150 | 155 | 160 |
| Glu | Val | Val | Pro | Pro | Arg | Ser | Asn | Asn | His | Ser | Gln | Leu | Ser | Leu | Asp | 165 | 170 | 175 | |
| Lys | Arg | Phe | Gln | Lys | Glu | Ala | His | Lys | Leu | Phe | Val | Asn | Lys | Arg | Gly | 180 | 185 | 190 | |
| Pro | Ile | Leu | Val | Met | Asp | Ala | Glu | Asn | Gly | Glu | Leu | Leu | Val | Ala | Gly | 195 | 200 | 205 | |
| Ser | Tyr | Pro | Glu | Tyr | Asn | Leu | Asn | Asp | Phe | Val | Gly | Gly | Ile | Ser | Gln | 210 | 215 | 220 | |
| Asp | Lys | Trp | Gln | Lys | Leu | Gln | Asp | Asp | Ile | Tyr | Asn | Pro | Leu | Leu | Asn | 225 | 230 | 235 | 240 |
| Arg | Phe | Ala | Asn | Ala | Leu | Tyr | Pro | Pro | Gly | Ser | Val | Val | Lys | Met | Gly | 245 | 250 | 255 | |
| Val | Gly | Leu | Ser | Phe | Leu | Glu | Asn | Leu | His | Ile | Thr | Glu | Asn | Thr | Thr | 260 | 265 | 270 | |
| Ile | Pro | Thr | Pro | Pro | Phe | Ile | Glu | Val | Gly | Lys | Arg | Lys | Phe | Arg | Asp | 275 | 280 | 285 | |
| Trp | Lys | Lys | Thr | Gly | His | Gly | Asn | Ser | Asn | Leu | Tyr | Lys | Ala | Ile | Arg | 290 | 295 | 300 | |
| Glu | Ser | Val | Asp | Val | Tyr | Phe | Tyr | Lys | Phe | Gly | Leu | Glu | Ile | Ser | Ile | 305 | 310 | 315 | 320 |
| Glu | Lys | Leu | Ser | Lys | Thr | Leu | Arg | Glu | Val | Gly | Phe | Gly | Glu | Lys | Thr | 325 | 330 | 335 | |
| Gly | Val | Asp | Leu | Pro | Asn | Glu | Phe | Val | Gly | Ile | Val | Pro | Asp | Asn | Leu | 340 | 345 | 350 | |
| Trp | Lys | Leu | Lys | Arg | Phe | Asn | Gln | Asp | Trp | Arg | Val | Gly | Asp | Thr | Leu | 355 | 360 | 365 | |
| Ile | Thr | Ala | Ile | Gly | Gln | Gly | Ser | Phe | Leu | Ala | Thr | Pro | Leu | Gln | Val | 370 | 375 | 380 | |
| Leu | Ala | Tyr | Thr | Gly | Leu | Ile | Ala | Thr | Gly | Lys | Leu | Ala | Thr | Pro | His | 385 | 390 | 395 | 400 |
| Phe | Ala | Ile | His | Asn | Gln | Gln | Pro | Leu | Lys | Asp | Pro | Leu | Asn | Ser | Phe | 405 | 410 | 415 | |
| Gln | Lys | Lys | Lys | Leu | Gln | Ala | Leu | Arg | Val | Gly | Met | Tyr | Glu | Val | Cys | 420 | 425 | 430 | |
| Asn | His | Lys | Asp | Gly | Thr | Ala | Tyr | His | Ser | Thr | Arg | Gly | Ser | Lys | Val | 435 | 440 | 445 | |
| Thr | Leu | Ala | Cys | Lys | Thr | Gly | Thr | Ala | Gln | Val | Val | Glu | Ile | Ala | Gln | 450 | 455 | 460 | |
| Asn | Ile | Val | Asn | Arg | Met | Lys | Glu | Lys | Asp | Met | Glu | Tyr | Phe | His | Arg | 465 | 470 | 475 | 480 |
| Ser | His | Ala | Trp | Ile | Thr | Ala | Phe | Leu | Pro | Tyr | Glu | Lys | Pro | Lys | Tyr | 485 | 490 | 495 | |

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Ala Ile Thr Ile Leu Val Glu His Gly Gly Gly Ser Lys Leu Gly
 500 505 510
 Gly Leu Leu Val Lys Met Ser Asn Lys Leu Tyr Glu Leu Gly Tyr Leu
 515 520 525

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773

Ile Asn Phe Val Asn Lys Gly Val Phe Met Asn Ile Phe Lys Arg Ile
 1 5 10 15
 Ile Cys Val Thr Ala Ile Val Leu Gly Phe Phe Asn Leu Leu Asp Ala
 20 25 30
 Lys His His Lys Glu Lys Lys Glu Asp His Lys Ile Thr Arg Glu Leu
 35 40 45
 Lys Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val
 50 55 60
 Val Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe
 65 70 75 80
 Thr Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp
 85 90 95
 Ala Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp
 100 105 110
 Arg Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu
 115 120 125
 Arg Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly
 130 135 140
 Ser Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu
 145 150 155 160
 Ile Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn
 165 170 175
 Leu Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys
 180 185 190
 Ile Lys Pro Leu Glu Ala Ala Leu Leu Pro Lys Val Leu Gly Asp Val
 195 200 205
 Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu Thr
 210 215 220
 Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu Val
 225 230 235 240
 Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu Ile
 245 250 255
 Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr Tyr
 260 265 270
 Lys Gly Ala Ile Ile Pro Ala Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:1774:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774

```

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1      5      10      15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
20      25      30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
35      40      45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
50      55      60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65      70      75      80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85      90      95
Ala Leu Ala Trp Asn Phe Trp Val Leu Leu Leu Ser Arg Met Gly Ile
100     105     110
Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser Leu Val Ile
115     120     125
Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly Leu Leu Ala
130     135     140
Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu Gly Arg Ile
145     150     155     160
Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val Ile Gly Gly
165     170     175
Val Ala Thr Leu Ile Met Leu Leu Met Trp Lys Leu Leu Pro His Leu
180     185     190
Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Ile Leu Met Lys
195     200     205
Arg Pro Leu Leu Val Gly Ile Tyr Leu Leu Val Ile Met Val Ile Ser
210     215     220
Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe Ile Ile Gln Ile
225     230     235     240
Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu Phe Val Phe Gly
245     250     255
Leu Ala Asp Val Val Gly Ser Phe Leu Phe Gly Arg Leu Tyr Ala Lys
260     265     270
Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro
275     280     285
Gln Leu Leu Leu Phe Val Phe Lys Asn Leu Glu Trp Val Ile Phe Leu
290     295     300
Gln Ile Phe Leu Trp Gly Ile Gly Ile Thr Ser Leu Thr Ile Thr Leu
305     310     315     320
Gln Asn Glu Gly Ile His
325

```

(2) INFORMATION FOR SEQ ID NO:1775:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775

```

Lys Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala
1          5          10          15
Phe Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr
20          25          30
Ala Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro
35          40          45
Leu Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys
50          55          60
Asn Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile
65          70          75          80
Ile Lys Ser Ser Ala Glu Thr Arg
85

```

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776

```

Arg Ile Ile Lys Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr
1          5          10          15
Ala Ser Leu Ile Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys
20          25          30
Glu Asn Gly Pro His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val
35          40          45
Cys Lys Ser Gly Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr
50          55          60
His Thr Gln Asp Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys
65          70          75          80
Pro Lys Ala Val Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu
85          90          95
Pro Thr Asn His Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn

```

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```

          100          105          110
Val His Phe His Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg
          115          120          125
Pro Leu Ser Ala His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu
          130          135          140
Val Leu Ala Ile Gly Phe
          145          150

```

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777

```

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1          5          10          15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
          20          25          30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
          35          40          45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
          50          55          60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65          70          75          80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
          85          90          95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
          100          105          110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
          115          120          125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
          130          135          140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145          150          155          160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
          165          170          175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
          180          185          190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
          195          200          205
Asn His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Ala Gly Ile
          210          215          220
Ala Ile Glu Ile Glu Ala Glu Cys Lys Thr Pro Lys Pro Thr Lys Thr
225          230          235          240
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro
          245          250          255
His Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln
          260          265          270
Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln
          275          280          285

```

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Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro
 290 295 300
 Arg Asp Phe Asn Ala Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile
 305 310 315 320
 Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu Lys Pro
 325 330 335
 Asp Pro Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Leu Val Gln
 340 345 350
 Lys Ile Phe Ala Asp Val Ser Lys Glu Ile Lys Val Val Ala Asn Thr
 355 360 365
 Glu Lys Lys Val Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
 370 375 380

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778

Asn Lys Arg Lys Asn Ile Lys Glu Val Tyr Ala Gly Glu Ile Cys Ala
 1 5 10 15
 Phe Val Gly Leu Lys Asp Thr Leu Thr Gly Asp Thr Leu Cys Asp Glu
 20 25 30
 Lys Asn Ala Val Val Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
 35 40 45
 His Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
 50 55 60
 Val Ala Leu Gly Lys Leu Ala Glu Glu Asp Pro Ser Phe Arg Val Met
 65 70 75 80
 Thr Gln Glu Glu Thr Gly Gln Thr Leu Ile Gly Gly Met Gly Glu Leu
 85 90 95
 His Leu Glu Ile Ile Val Asp Arg Leu Lys Arg Glu Phe Lys Val Glu
 100 105 110
 Ala Glu Ile Gly Gln Pro Gln Val Ala Phe Arg Glu Thr Ile Arg Ser
 115 120 125
 Ser Val Ser Lys Glu His Lys Tyr Ala Lys Gln Ser Gly Gly Arg Gly
 130 135 140
 Gln Tyr Gly His Val Phe Ile Lys Leu Glu Pro Lys Glu Pro Gly Ser
 145 150 155 160
 Gly Tyr Glu Phe Val Asn Glu Ile Ser Gly Gly Val Ile Pro Lys Glu
 165 170 175
 Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Ala Met Gln Asn Gly
 180 185 190
 Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu Tyr Asp
 195 200 205
 Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys Ile Ala
 210 215 220
 Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro Val Leu
 225 230 235 240
 Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu Tyr Met

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| | | | | | |
|---|---|--|-----|--|-----|
| | 245 | | 250 | | 255 |
| Gly Asp Val Ile | Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile Asn Ser | | | | |
| | 260 | | 265 | | 270 |
| Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val Pro Leu | | | | | |
| | 275 | | 280 | | 285 |
| Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr Gln Gly | | | | | |
| | 290 | | 295 | | 300 |
| Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val Pro Ser | | | | | |
| 305 | 310 | | 315 | | 320 |
| Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly | | | | | |
| | 325 | | 330 | | |

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779

| | | |
|---|-----|-------|
| Ser Lys Arg Ala Phe Ala Ser Ser Leu Val Ser Ser Lys Leu Phe Leu | | |
| 1 | 5 | 10 15 |
| Arg Asp Lys Glu Thr Arg Lys Arg Gly Leu Glu Thr Val Gly Gly Arg | | |
| | 20 | 25 30 |
| Ile Ala Pro Thr Lys Asn Pro Phe Ser Phe Lys Lys Tyr Trp Ala Phe | | |
| | 35 | 40 45 |
| Lys Arg Ala Gly Leu Phe Ser Asn Ser Arg Val Lys Asn Pro Val Gly | | |
| | 50 | 55 60 |
| Val Leu Thr Pro Lys Val Ser Lys Ile Ile Cys Trp Cys Leu Leu Ser | | |
| 65 | 70 | 75 80 |
| Ser Phe Phe Asn Ser Cys Phe Cys Ala Ile Lys Tyr Ser Lys Trp Ala | | |
| | 85 | 90 95 |
| Lys Val Lys Ala Val Ser Asn Arg Leu Lys Ala Val Val | | |
| | 100 | 105 |

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780

```

Ile Arg Asn Ala Thr Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile
1      5      10      15
Ser Gln Lys Asp Ser Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu
20      25      30
Tyr Gln Ser Leu Leu Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile
35      40      45
Lys Asn Asn Lys Val Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn
50      55      60
Asn Leu Glu Glu Gln Ser Val His Phe Lys Glu Asn Ala Glu Ser Val
65      70      75      80
Asn Leu Gln Gly Val Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly
85      90      95
Val Gln Tyr Phe Ser Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr
100      105      110
His Lys Asn Asp Leu Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly
115      120      125
Leu Glu Asn Ala Gln Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly
130      135      140
Leu Leu Leu Asn Ala Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly
145      150      155      160
Leu Ile Thr Val Asn Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu
165      170      175
Lys Met Gln Asn Ala Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser
180      185      190
Asn Glu Ile Thr Gln Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln
195      200      205
Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly
210      215      220
Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu
225      230      235      240
Ala Glu Lys Thr Gln Lys Ala Thr Lys Glu Ile Ala Val Val Val Lys
245      250      255
Ser Met Gln Gln Glu Ala Asn Asp Ile Gln Thr Asn Thr His Asp Ile
260      265      270
Asn Ser Ile Val Gly Ser Ile Lys Gly Asp Val Glu Glu Leu Lys Ser
275      280      285
Thr Val Lys Asn Asn Met Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile
290      295      300
Tyr Asn Ile Asn Asn Arg Val Phe Cys Gly Leu Ala Lys Leu Asp His
305      310      315      320
Val Val Phe Lys Asn Asn Leu Tyr Gly Met Val Phe Gly Leu Asn Ser
325      330      335
Phe Asp Ile Thr Ser His Lys Ser Cys Arg Leu Gly Lys Trp Tyr Tyr
340      345      350
Glu Gly Ala Gly Lys Glu Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala
355      360      365
Leu Glu Ser His His Ala Ser Val His Ala Glu Ala Asn Asp Leu Val
370      375      380
Lys Ala Val Gln Glu Asp His Val Thr Asp Ser Lys Tyr Leu Glu His
385      390      395      400
Lys Val His Leu Met Glu Asp Ser Ala Lys His Val Lys Glu Asn Ile
405      410      415
Asp Lys Met Phe Tyr Glu Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu
420      425      430
Lys Ile Gln Lys Gly Glu
435

```

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781

```

Glu Trp Leu Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe
1      5      10      15
Leu Ile Ile Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val
20      25      30
Thr Thr Asp Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val
35      40      45
Ala Ser Gln Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr
50      55      60
Asp Lys Glu Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg
65      70      75      80
Phe Val Glu Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His
85      90      95
Gly Gly Ile Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala
100     105     110
Lys Ser Gly Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu
115     120     125
Val Lys Asn Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu
130     135     140
Lys Glu Ala Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu
145     150     155     160
Glu Ile Leu Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr
165     170     175
Tyr Gly Val Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp
180     185     190
Lys Leu Thr Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala
195     200     205
Pro Ser Phe Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg
210     215     220
Ala Asn Asp Ile Leu Arg Arg Leu Tyr Ser Leu Gly Trp Ile Ser Ser
225     230     235     240
Asn Glu Leu Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln
245     250     255
Thr Ser Thr Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys
260     265     270
Gln Leu Asp Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys
275     280     285
Leu Thr Ile Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg
290     295     300
Phe Gly His Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys
305     310     315     320
Thr Asn Ala Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Gln His
325     330     335
Asp Ser Tyr Arg Asn Glu His Arg
340

```

(2) INFORMATION FOR SEQ ID NO:1782:

SUBSTITUTE SHEET (RULE 26)

1317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782

```

Ile Arg Thr Pro Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe
1      5      10      15
Ile Leu Leu Tyr Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile
20      25      30
Thr Val Leu Phe Val Gly Ile Leu Pro Ser Leu Asn Ile Leu Val Met
35      40      45
Ile Lys Leu Ile Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His
50      55      60
Phe Glu Tyr Ser Leu Leu Pro Thr Leu Leu Trp Gly Ala Leu
65      70      75      80
Leu Phe Leu Thr His Val Phe Ser Gly Ile Leu Ser Ser Leu Gln Thr
85      90      95
Ile Ile Ala Glu Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn
100     105     110
Lys Leu Thr Gln Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His
115     120     125
Thr Ile Lys Leu Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu
130     135     140
Asn Tyr Val Ser Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu
145     150     155     160
Ile Ser Leu Phe Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe
165     170     175
Ile Met Ile Phe Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile
180     185     190
Ala Lys Lys His Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu
195     200     205
Ser Met Gln Asn Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys
210     215     220
Asp Asn Leu Leu Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile
225     230     235     240
Glu Thr Lys Glu Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys
245     250     255
Asn Leu Ile Phe Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser
260     265     270
Ile Ala Leu Phe Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile
275     280     285
Gly Val Gly Ala Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln
290     295     300
Gln Gln Leu Gln Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile
305     310     315     320
Asn Lys Tyr Phe Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro
325     330     335
Lys Pro Glu Thr Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr
340     345     350
Phe Glu Asn Ile Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu
355     360     365
Asn Phe Asn Leu Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly

```

SUBSTITUTE SHEET (RULE 26)

1318

```

      370              375              380
Lys Asn Ala Ser Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe
385              390              395              400
Tyr Thr Pro Asn Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu
      405              410              415
Gln Asp Leu Glu Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe
      420              425              430
Gln Asp Phe Ser Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe
      435              440              445
Met Gln Asn Asn Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile
      450              455              460
Leu Lys Ser Phe Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn
465              470              475              480
Asn Thr Leu Phe Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly
      485              490              495
Gln Lys Gln Arg Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn
      500              505              510
Cys Ile Val Leu Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu
      515              520              525
Lys Glu Phe Leu Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala
      530              535              540
Leu Ile Ile Thr His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile
545              550              555              560
Ile Val Leu Asp Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr
      565              570              575
Leu Met Lys Lys Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln
      580              585              590
Tyr

```

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783

```

Thr Pro Ser Met Ile Val Thr Glu Thr Ser Thr Gly Lys Ile Leu Ala
1              5              10              15
Leu Val Gly Gly Ile Asp Tyr Lys Lys Ser Ala Phe Asn Arg Ala Thr
      20              25              30
Gln Ala Lys Arg Gln Phe Gly Ser Ala Ile Lys Pro Phe Val Tyr Gln
      35              40              45
Ile Ala Phe Asp Asn Gly Tyr Ser Thr Thr Ser Lys Ile Pro Asp Thr
      50              55              60
Ala Arg Asn Phe Glu Asn Gly Asn Tyr Ser Lys Asn Ser Val Gln Asn
      65              70              75              80
His Ala Trp His Pro Ser Asn Tyr Thr Arg Lys Phe Leu Gly Leu Val
      85              90              95
Thr Leu Gln Glu Ala Leu Ser His Ser Leu Asn Leu Ala Thr Ile Asn
      100              105              110

```

SUBSTITUTE SHEET (RULE 26)

1319

Leu Ala Ile Ala Trp
115

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Gln | Gly | Val | Thr | Thr | Met | Ala | Phe | Gln | Val | Asn | Thr | Asn | Ile | Asn | Ala | 1 | 5 | 10 | 15 |
| Met | Asn | Ala | His | Val | Gln | Ser | Ala | Leu | Thr | Gln | Asn | Ala | Leu | Lys | Thr | 20 | 25 | 30 | |
| Ser | Leu | Glu | Arg | Leu | Ser | Ser | Gly | Leu | Arg | Ile | Asn | Lys | Ala | Ala | Asp | 35 | 40 | 45 | |
| Asp | Ala | Ser | Gly | Met | Thr | Val | Ala | Asp | Ser | Leu | Arg | Ser | Gln | Ala | Ser | 50 | 55 | 60 | |
| Ser | Leu | Gly | Gln | Ala | Ile | Pro | Asn | Thr | Asn | Asp | Gly | Met | Gly | Ile | Ile | 65 | 70 | 75 | 80 |
| Gln | Val | Ala | Asp | Lys | Ala | Met | Asp | Glu | Gln | Leu | Lys | Ile | Leu | Asp | Thr | 85 | 90 | 95 | |
| Val | Lys | Val | Lys | Ala | Thr | Gln | Ala | Ala | Gln | Asp | Gly | Gln | Thr | Thr | Glu | 100 | 105 | 110 | |
| Ser | Arg | Lys | Ala | Ile | Gln | Ser | Asp | Ile | Val | Arg | Leu | Ile | Gln | Gly | Leu | 115 | 120 | 125 | |
| Asp | Asn | Ile | Gly | Asn | Thr | Thr | Tyr | Asn | Gly | Pro | Ser | Val | Ile | Val | | 130 | 135 | 140 | |
| Trp | Ser | Ile | His | | | | | | | | | | | | | 145 | | | |

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785

SUBSTITUTE SHEET (RULE 26)

1320

```

Phe Lys Val Trp Ile Ile Ser Val Thr Gln Arg Leu Ile Thr Gly Gln
1      5      10      15
Ala Leu Leu Ser Gly Gln Phe Thr Asn Lys Glu Phe Gln Val Gly Ala
20      25      30
Tyr Ser Asn Gln Ser Ile Lys Ala Ser Ile Gly Ser Thr Thr Ser Asp
35      40      45
Lys Ile Gly Gln Val Arg Ile Ala Thr Gly Ala Leu Ile Thr Ala Ser
50      55      60
Gly Asp Ile Ser Leu Thr Phe Lys Gln Val Asp Gly Val Asn Asp Val
65      70      75      80
Thr Leu Glu Ser Val Lys Val Ser Ser Ser Ala Gly Thr Gly Ile Gly
85      90      95
Val Leu Ala Glu Val Ile Asn Lys Asn Ser Asn Arg Thr Gly Val Lys
100     105     110
Ala Tyr Ala Ser Val Ile Thr Thr Ser Asp Val Ala Val Gln Ser Gly
115     120     125
Ser Leu Ser Asn Leu Thr Leu Asn Gly Ile His Leu Gly Asn Ile Ala
130     135     140
Asp Ile Lys Lys Asn Asp Ser Asp Gly Arg Leu Val Thr Ala Ile Asn
145     150     155     160
Ala Val Thr Ser Glu Thr Gly Val Glu Ala Tyr Thr Asp Gln Lys Gly
165     170     175
Arg Leu Asn Leu Arg Ser Ile Asp Gly Arg Gly Ile Glu Ile Lys Ile
180     185     190
Asp Ser Val Ser Asn Gly Pro Ser Ala Leu Thr Lys Arg Trp Ser Lys
195     200     205
Ser Gly Gln Asp Glu Thr Lys Gly Ser Thr Asn Tyr Gly Arg Tyr Ser
210     215     220
Arg Thr Arg Leu Asp Val Arg Ala Ser Met Ser Ile Arg Tyr Leu Asn
225     230     235     240
His Ala Cys Leu Leu Gln Ser Tyr
245

```

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786

```

Ser Pro Leu Trp Leu Lys Thr Arg Phe Pro Asn Ile Trp Leu Ala Lys
1      5      10      15
Ile Leu Tyr Met Ala Ile Leu Leu Cys Ala Ile Ala His Ser Val Gly
20      25      30
Leu Ile Leu Arg Trp Tyr Val Ser Gly His Ser Pro Trp Ser Asn Ala
35      40      45
Tyr Glu Ser Met Leu Tyr Ile Ala Trp Ala Ser Val Ile Ala Gly Phe
50      55      60
Val Leu Arg Ser Lys Leu Ala Leu Ser Ala Ser Ser Phe Leu Ala Gly
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

1321

```

Ile Ala Leu Phe Val Ala His Leu Gly Phe Met Asp Pro Gln Ile Gly
      85          90          95
Pro Leu Val Pro Val Leu Lys Ser Tyr Trp Leu Asn Ile His Val Ser
      100        105        110
Val Ile Thr Ala Ser Tyr Gly Phe Leu Gly Leu Cys Phe Val Leu Gly
      115        120        125
Ile Leu
      130

```

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787

```

Lys Arg Leu Glu Met Gly Leu Ser Val Gly Ile Val Gly Leu Pro Asn
1      5      10      15
Val Gly Lys Ser Ser Thr Phe Asn Ala Leu Thr Lys Thr Gln Asn Ala
      20      25      30
Gln Ser Ala Asn Tyr Pro Phe Cys Thr Ile Glu Pro Asn Lys Ala Ile
      35      40      45
Val Asn Val Pro Asp Arg Arg Leu Asp Ala Leu Ala Gln Ile Val Lys
      50      55      60
Pro Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly
      65      70      75      80
Leu Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu
      85      90      95
Ala Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe
      100     105     110
Glu Asp Asp Asn Ile Thr His Val Asn Asp Lys Ile Asp Pro Leu Asn
      115     120     125
Asp Ile Glu Thr Ile Glu Leu Glu Leu Ile Leu Ala Asp Ile Ala Thr
      130     135     140
Leu Asp Lys Arg Ile Asp Arg Leu Gln Lys Ala Leu Lys Ser Ser Lys
      145     150     155     160
Asp Ala Lys Asn Leu Leu Glu Cys Ala Leu Ser Leu Lys Thr His Leu
      165     170     175
Glu Glu Leu Lys Pro Ala Lys Thr Phe Pro Leu Asn Thr Ser Glu Ala
      180     185     190
Phe Leu Glu Leu Asp Lys Glu Leu Arg Phe Leu Ser His Lys Lys Met
      195     200     205
Ile Tyr Val Ala Asn Val Gly Glu Glu Asp Leu Asn Ile Leu Asn Glu
      210     215     220
His Ala Lys Lys Val Glu Asn His Ala Lys Val Gln Asn Ser Glu Phe
      225     230     235     240
Val Ala Leu Cys Ala Lys Leu Glu Glu Glu Met Val Ser Met Ser Gly
      245     250     255
Asp Glu Val Lys Glu Phe Leu Gln Ser Leu Gly Val Glu Glu Ser Gly
      260     265     270
Leu Glu Lys Thr Ile Arg Leu Ser Phe Lys Glu Leu Gly Leu Ile Asn

```

SUBSTITUTE SHEET (RULE 26)

1322

```

      275      280      285
Tyr Phe Thr Ala Gly Val Lys Glu Val Arg Ser Trp Thr Ile Lys Lys
290      295      300
Gly Ser Ser Ala Pro Val Ala Ala Gly Val Ile His Lys Asp Phe Glu
305      310      315      320
Lys Gly Phe Ile Arg Ala Glu Thr Ile Ser Tyr Asp Asp Phe Ile Ala
      325      330      335
Tyr Lys Gly Glu Ala Gly Ala Lys Glu Lys Gly Ala Leu Arg Ile Glu
      340      345      350
Gly Lys Asp Tyr Ile Val Gln Asp Gly Asp Val Leu His Phe Arg Phe
      355      360      365
Asn Val
370

```

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788

```

Arg Asn Lys Thr Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr
1      5      10      15
Lys Leu Gln Asn Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile
      20      25      30
Ile Phe Ile Trp Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu
      35      40      45
Gly Ile Ala Pro Phe Val Ala Asn Ser Pro Phe Phe Ser Phe Met Tyr
      50      55      60
Lys Phe Glu Lys Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln
      65      70      75      80
Ser Met Gln Glu Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys
      85      90      95
Glu Trp His Lys Glu Asn Arg Thr Tyr Leu Val Ala Glu Gly Leu Gly
      100      105      110
Ile Thr Ile Met Ile Leu Gly Ile Leu Val Leu Leu Gly Leu Trp Met
      115      120      125
Pro Leu Met Gly Val Val Gly Gly Phe Leu Ser Leu Glu
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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1323

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789

```

Arg Ser Pro Pro Tyr Ser Phe Leu Phe Thr Thr Pro Glu Val Phe Val
1      5      10      15
Asn Gln His Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val Lys
20      25      30
Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp Ala
35      40      45
Lys Arg Tyr Leu Glu Gly Lys Gly Phe Cys Leu Met Asp Arg Ser Ser
50      55      60
Val Gly Ile Lys Thr Lys Cys Ser Ser Gly Cys Cys Ser
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790

```

Trp Cys Phe Thr Asn Ile Gln Glu Ile Gly Asn Asp Phe Leu Ile Pro
1      5      10      15
Gln Ser Phe Lys Lys Lys Asp Phe Ser Asn Leu Ala Gln Gln Val Cys
20      25      30
His Arg His Glu Gly Phe Gly Ala Asp Gly Leu Val Val Leu Pro
35      40      45
Ser Lys Asp Tyr Asp Tyr Glu Trp Asp Phe Tyr Asn Ser Asp Gly Ser
50      55      60
Lys Ala Gly Met Cys Gly Asn Ala Ser Arg Cys Val Gly Leu Phe Ala
65      70      75      80
Tyr Gln His Ala Ile Ala Pro Lys Glu His Val Phe Leu Ala Gly Lys
85      90      95
Arg Glu Ile Ser Ile Arg Ile Glu Glu Pro Asn Ile Val Glu Ser Asn
100     105     110
Leu Gly Asn Tyr Gln Ile Leu Asp Thr Ile Pro Asn Leu Arg Cys Lys
115     120     125
Lys Phe Phe Thr Asn Asn Ser Val Leu Glu Asn Ile Pro Met Phe Tyr
130     135     140
Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val Lys Asn Lys
145     150     155     160
Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala Leu Arg His
165     170     175
Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn Lys Glu Thr

```

SUBSTITUTE SHEET (RULE 26)

1324

```

      180      185      190
Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe Thr Leu Ala
      195      200      205
Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg Leu Phe His
      210      215      220
Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn Glu Phe Leu
      225      230      235      240
Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly Val Ala Arg
      245      250      255
Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys Asn Gly Cys
      260      265      270
Phe

```

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791

```

Phe Leu Val Gln Phe Asn Gly Asp Asn Cys Met Lys Ala Gln Tyr Phe
1      5      10      15
Phe Trp Ile Leu Phe Leu Ile Gly Phe Tyr Trp Met Leu Tyr Leu Tyr
      20      25      30
Gln Asp Phe Leu Met Asp Ala Leu Ile Ala Gly Leu Leu Cys Val Gly
      35      40      45
Leu Phe Gln Val Lys Val Phe Leu Asn Lys Arg Phe Ser Asn Val Ile
      50      55      60
Ser Ser Phe Leu Cys Val Leu Val Leu Ala Ser Val Val Ile Val Pro
      65      70      75      80
Leu Tyr Phe Ile Val Tyr Lys Gly Ser Asn Val Ile Phe Glu Ile Asn
      85      90      95
Phe Glu Lys Leu Ser Ala Leu Ile Lys Trp Leu Lys Gly Thr Ile Thr
      100      105      110
Glu Asn Leu Ser His Phe Pro Ala Ile His Asp Gly Val Ser Lys Phe
      115      120      125
Leu Glu Asn Phe Ser Ala Ala Ser Ile Thr Gly Tyr Leu Leu Lys Val
      130      135      140
Ser Ser Tyr Ile Gly Lys Tyr Ser Leu Lys Leu Val Thr Asp Ala Leu
      145      150      155      160
Phe Ile Leu Gly Leu Leu Phe Phe Phe Phe Tyr Tyr Gly Glu Lys Phe
      165      170      175
Tyr Arg Tyr Phe Leu Gly Val Leu Pro Leu Glu Met Asn Gln Ser Lys
      180      185      190
Lys Ile Phe Glu Glu Val Ala Gly Ile Leu Arg Ile Val Leu Leu Thr
      195      200      205
Ser Leu Ile Thr Val Ile Leu Glu Gly Val Ala Phe Gly Thr Met Ile
      210      215      220
Ile Trp Phe Gly His Asp Gly Trp Ser Leu Gly Ile Leu Tyr Gly Leu
      225      230      235      240

```

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Ala Ser Leu Val Pro Ala Val Gly Gly Ala Leu Ile Trp Ile Pro Ile
 245 250 255
 Ala Ile Tyr Glu Leu Tyr His Gly His Val Asn Glu Ala Ile Phe Ile
 260 265 270
 Val Leu Tyr Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile
 275 280 285
 Lys Pro Ile Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr
 290 295 300
 Leu Lys Ile Asn Glu Ile Leu Ile Phe Phe Ser Met Ile Ala Gly Ile
 305 310 315 320
 Ser Gln Phe Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala
 325 330 335
 Phe Phe Ile Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys
 340 345 350
 Glu Gln Lys Thr Cys Glu Cys
 355

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792

Arg Leu Asn Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr
 1 5 10 15
 Leu Leu Phe Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys
 20 25 30
 Ile Ala Lys Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe
 35 40 45
 Asn Asn Lys Pro Ile Asn Thr Asn Lys Gly Ile Tyr Pro Thr Glu Thr
 50 55 60
 Phe Met Thr Ile Met Ala Tyr Met Gln Val Asp Phe Thr Glu Leu Leu
 65 70 75 80
 Pro Lys Ser Ala Thr Ala Asn Gly His His Leu Asp Gly Ser Leu Gly
 85 90 95
 Gly Trp Gly Gly Ala Val Ile Tyr Asp Ser Thr Lys Asp Phe Ile Asn
 100 105 110
 Glu Val Thr Gly Lys Pro Tyr Gly Ala Met Thr Trp Asn Tyr Val Gly
 115 120 125
 Tyr Trp Gly Gly Leu Val Gly Gln Lys Pro Trp Ala Ser Cys Gly Leu
 130 135 140
 Ala Thr Gly Asn Leu Thr Gln Gly Gln Tyr Asp Lys Met Thr Gln Ala
 145 150 155 160
 Glu Met Thr Gln Leu Ser Asn Gln Glu Ala Leu Ala Ala Ser Thr Cys
 165 170 175
 Ala Lys Thr Tyr Ala Asp His Thr Arg Asn Tyr Val Ile Tyr Asn Ala
 180 185 190
 Tyr Leu Arg Tyr Asn Tyr Lys Asp Ile Phe Glu Ile Arg Gly Gly Arg
 195 200 205
 Tyr Glu Ser Gln Arg Ile Ile

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1326

210

215

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793

```

Ile Phe Tyr Pro Asn Gly Tyr Asn Asn Arg Met Gly Phe Leu Lys Val
1      5      10      15
Leu Lys His Asp Ala Leu Gly Gln Val Gly Asn Ile Val Ile Gly Asn
20      25      30
Phe Leu Ile Thr Leu Thr Val Leu Ala Val Cys Phe Ser Ser Gln Ser
35      40      45
Ala Glu Glu Thr Thr Met Leu Thr Leu Ser Tyr Thr Leu Phe Phe Ile
50      55      60
Leu Gly Ala Phe Leu Leu Val Ala Ile Ser Val Gly Ala Ile Lys Asn
65      70      75      80
Leu Asn Ala Leu Phe Ser Lys Arg Gly Val Leu Ser Phe Ser Leu Pro
85      90      95
Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys Ile Leu Leu Pro Met Val
100     105     110
Phe Phe Ile Phe Ser Leu Phe Trp Phe Val Ala Ser Val Arg Leu Gly
115     120     125
Tyr Tyr Leu Phe Asn Ala Gln Ser Ser Val Leu Phe Ile Leu His Thr
130     135     140
Ala Leu Lys Thr Phe Ala Leu Lys Pro Thr Lys Thr Ile Gly Val Ala
145     150     155     160
Leu Phe Leu Gly Leu Val Leu Met Lys Phe Leu Phe Val Leu Ser Val
165     170     175
Leu Asn Ala Thr Arg Ile Lys Lys Ala Arg Phe Leu Leu Gly Gly Leu
180     185     190
Leu Phe Ile Leu Val Gly Val Val Leu Glu Leu Ala Phe Asn Ser Leu
195     200     205
Leu Pro Leu Met Ser Ser Ser Leu Ser Ile Asn Glu Gly Phe Tyr Tyr
210     215     220
Phe Leu Gln Gln Gln Glu Leu Gln Glu Asn Lys Tyr Tyr Leu Leu Trp
225     230     235     240
Gly Val Asp Phe Leu Lys Ile Leu Leu Leu Tyr Gly Val Ile Arg Tyr
245     250     255
Leu Leu Thr His Lys Leu Glu Leu Asp
260     265

```

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794

```

His Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe
1      5      10      15
Leu Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu
20     25     30
Thr Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr
35     40     45
Leu Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys
50     55     60
Asn Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu
65     70     75     80
Gly Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr
85     90     95
His Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu
100    105    110
Asp Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr
115    120    125
Asn Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn
130    135    140
Gly Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn
145    150    155    160
Ile Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val
165    170    175
Val Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu
180    185    190
Tyr Phe Phe Lys Lys Ser
195

```

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795

```

Glu Gly Lys Ser Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met
1      5      10      15
Ser Val Leu Ile Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe

```

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```

      20      25      30
Ala Leu Lys Asn Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His
      35      40      45
Asn Glu Val Asp Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn
      50      55      60
Phe Lys Ser Asn Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu
      65      70      75      80
Ser Pro Lys Thr Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly
      85      90      95
Asp Lys Lys Ile Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu
      100      105      110
Lys Ser Asn Thr Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu
      115      120      125
Asp Ser Pro Asn Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser
      130      135      140
Gln Pro Arg Leu Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro
      145      150      155      160
Leu Lys Phe Asp Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile
      165      170      175
Leu Phe Lys Phe Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln
      180      185      190
Leu Ala Phe Phe Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796

```

Ala Asn Gln Phe Ala Leu Gln Phe Ser Phe Ser Asn Phe Lys His Gly
1      5      10      15
Asp Phe Thr Thr Arg Asp Phe Met Leu Tyr Ser Leu Leu Tyr Gly Tyr
      20      25      30
Phe Asn Ile Asn Leu Phe Gln Tyr Leu Thr Phe Arg Ala Gly Leu Gly
      35      40      45
Phe Phe Ile Ala Phe Phe Leu Thr Leu Phe Leu Met Pro Lys Phe Ile
      50      55      60
Leu Trp Ala Lys Ala Lys Lys Ala Asn Gln Pro Ile Ser Ser Phe Val
      65      70      75      80
Pro Ser His Gln Asn Lys Lys Asp Thr Pro Thr Met Gly Gly Ile Val
      85      90      95
Phe Val Phe Ala Thr Ile Val Ala Ser Val Leu Cys Ala Ser Leu Ser
      100      105      110
Asn Leu Tyr Val Leu Leu Gly Ile Ile Val Leu Val Gly Phe Ser Phe
      115      120      125
Val Gly Phe Arg Asp Asp Tyr Thr Lys Ile Asn Gln Gln Asn Asn Ala
      130      135      140
Gly Met Ser Ala Lys Met Lys Phe Gly Met Leu Phe Ile Leu Ser Leu
      145      150      155      160

```

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```

Ile Val Ser Val Leu Leu Ser Leu Lys Gly Leu Asp Thr Phe Leu Tyr
      165      170      175
Ala Pro Phe Leu Lys Asn Pro Leu Phe Glu Met Pro Thr Met Leu Ala
      180      185      190
Val Gly Phe Trp Val Leu Val Phe Leu Ser Thr Ser Asn Ala Val Asn
      195      200      205
Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser Val Pro Ser Ile Phe Thr
      210      215      220
Leu Leu Ser Leu Ser Ile Phe Val Tyr Val Ala Gly Asn Ala Glu Phe
      225      230      235      240
Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile Asp Val Gly Glu Leu Phe
      245      250      255
Val Ile Ser Leu Ala Leu Val Gly Ser Leu Phe Gly Phe Leu Trp Tyr
      260      265      270
Asn Cys Asn Pro Ala Ser Val Phe Met Gly Asp Ser Gly Ser Leu Ala
      275      280      285
Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile Val Ser His Asn Glu Ile
      290      295      300
Leu Leu Val Leu Met Gly Ser Ile Phe Val Ile Glu Thr Leu Ser Val
      305      310      315      320
Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg Lys Lys Arg Leu Phe Leu
      325      330      335
Met Ala Pro Ile His His His Phe Glu Gln Lys Gly Trp Ala Glu Asn
      340      345      350
Lys Val Ile Val Arg Phe Trp Ile Ile Ser Met Leu Ser Asn Leu Val
      355      360      365
Ala Leu Leu Ser Leu Lys Val Cys
      370      375

```

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797

```

Ala Arg Phe Ile Lys Ile Phe Gly Met Gly Lys Phe Ser Lys Leu Gly
1      5      10      15
Phe Ile Leu Ala Thr Leu Gly Ser Ser Ile Gly Leu Gly His Ile Trp
      20      25      30
Arg Phe Pro Tyr Met Val Gly His Asn Gly Gly Ser Ala Phe Val Leu
      35      40      45
Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu Leu Val
      50      55      60
Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser Asn Tyr
      65      70      75      80
Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr Ser Phe
      85      90      95
Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val Val Leu
      100      105      110
Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu Pro Lys

```

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```

      115              120              125
Asp Leu Glu Gln Ala Lys Met Gln Phe Ser Met Leu Gln Asn Gly Ser
  130              135              140
Leu Ile Trp Pro Val Ile Gly Phe Ser Ala Cys Leu Leu Pro Thr Ile
  145              150              155              160
Trp Phe Val Ser Arg Gly Ile Glu Glu Gly Ile Glu Lys Leu Asn Val
      165              170              175
Val Leu Met Pro Leu Leu Phe Val Ile Phe Ile Gly Leu Leu Ile Tyr
      180              185              190
Ala Met Thr Leu Glu Ser Met Pro Lys Ala Leu Arg Phe Leu Phe Asn
      195              200              205
Phe Glu Ile Gln Lys Ile Asp Phe Lys Val Val Met Asp Ala Leu Gly
  210              215              220
Gln Met Phe Phe Ser Leu Ser Leu Gly Val Gly Thr Ile Ile Thr Tyr
  225              230              235              240
Ser Ala Phe Thr Pro Lys Lys Glu Asn Leu Lys Ser Ser Leu Phe
      245              250              255
Ile Val Leu Pro Gly Ile Leu Ile Ser Leu Ile Ala Gly Val Met Ile
      260              265              270
Phe Thr Phe Val Phe Glu Tyr His Ala Asp Val Ser Gln Gly Pro Gly
      275              280              285
Leu Val Phe Ile Ser Leu Pro Leu Thr Phe Ala Lys Met Gly Ser
      290              295              300

```

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798

```

Arg Cys Val Lys Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr
  1           5           10           15
Leu Ala Leu Gly Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe
      20           25           30
Phe Asp Asp Lys Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu
      35           40           45
Cys Tyr Pro Ser Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile
      50           55           60
Val Ser Pro Gly Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys
      65           70           75           80
His Leu Met Ser Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser
      85           90           95
Phe Thr Pro Thr Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr
      100          105          110
Thr Thr Glu Met Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser
      115          120          125
Gly Gly Asn Ile Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser
      130          135          140
Pro Leu Trp Val Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn
      145          150          155          160

```

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Lys Ala Tyr Pro Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His
 165 170 175
 Leu Thr Trp His Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys
 180 185 190
 Val Leu Thr Leu Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys
 195 200 205
 Phe Lys Glu His Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe
 210 215 220
 Phe Asp Lys Ser Glu Glu Val Leu Glu Cys Leu Lys Ile Pro Ser Asn
 225 230 235 240
 Ala Leu Phe Phe Lys Gly Ala Phe Leu Leu Asp Ala Ala Leu Ala Leu
 245 250 255
 Leu Val Tyr Glu Gln Phe Leu Lys Ile Lys Asn Leu Lys Trp Gln Asp
 260 265 270
 Tyr Arg Glu Asn Ala Leu Lys Arg Leu Asn Ala Phe Lys Ile Gly Ser
 275 280 285
 His Lys Met Glu Glu Phe Arg Asp Lys Gln Gly Arg Leu Trp Val Asp
 290 295 300
 Asp Ser Lys Ala Thr Asn Ile Asp Ala Thr Leu Gln Ala Leu Lys Thr
 305 310 315 320
 Phe Lys Asn Gln Lys Ile His Leu Ile Leu Gly Gly Asp Ile Lys Gly
 325 330 335
 Val Asn Leu Thr Pro Leu Phe Glu Glu Phe Lys Asn Tyr Lys Ile Ser
 340 345 350
 Leu Tyr Ala Ile Gly Ser Ser Ala Ser Ile Ile Gln Ala Leu Ala Leu
 355 360 365
 Glu Phe Asn Val Ser Cys Gln Val Cys Leu Lys Leu Glu Lys Ala Val
 370 375 380
 Gln Glu Ile Lys Ser Val Leu Leu Gln Asn Glu Val Ala Leu Leu Ser
 385 390 395 400
 Pro Ser Ala Ala Ser Leu Asp Gln Phe Ser Ser Tyr Lys Glu Arg Gly
 405 410 415
 Glu Lys Phe Lys Ala Phe Val Leu Lys Asp
 420 425

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799

Asp Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu
 1 5 10 15
 Gly Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr
 20 25 30
 Gly Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser
 35 40 45
 Leu Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln
 50 55 60
 Ser Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn

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```

65      70      75      80
Pro Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro
      85      90      95
Leu Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr
      100     105     110
Leu Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu
      115     120     125
Gln Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly
      130     135     140
Leu Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile
145     150     155     160
Lys Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe
      165     170     175
Ala Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe
      180     185     190
Ser Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr
      195     200     205
Ser Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser
      210     215     220
Ile Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr
225     230     235     240
Gln Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu
      245     250     255
Ile Ser Leu Val Gly Arg Ala Tyr Asp Phe His Phe Cys Val
      260     265     270

```

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800

```

Cys Leu Thr Arg His Arg Val Asn Leu His Phe Phe Thr Gly Gly Phe
1      5      10      15
Trp Pro Asn Gly Ser Asp Arg Arg Ser Cys Phe Asn Ser Phe Leu Ala
      20      25      30
Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg Ala
      35      40      45
Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
50      55      60

```

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801

```

Phe Leu Leu Trp Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr
1      5      10      15
Gly Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro
      20      25      30
Val Val Phe Gly Gln Met Gly Ala Ile Gly Val Leu Val Ser Ile Leu
      35      40      45
Phe Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu
50      55      60
Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln Tyr Ser Arg
65      70      75      80
Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val
      85      90      95
Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe
      100     105     110
Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile
      115     120     125
Ile Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val
130     135     140
Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe Leu Gly Pro
145     150     155     160
Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu
      165     170     175
Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
      180     185

```

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802

```

Glu Ser Phe Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr
1      5      10      15
Ser Lys Met Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys
      20      25      30
Ala Met Asn Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn
      35      40      45
Gln Gln Pro Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His

```

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```

      50              55              60
Val Thr Pro Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro
65              70              75              80
Gln Asn His His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser
      85              90              95
Asp Asn Leu Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn
      100             105             110
Gln Ile Gln Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe
      115             120             125
Gln Asp Glu Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser
      130             135             140
Val Leu Asp Leu Lys Gly Trp Val Gly Ile Leu Glu Asp Leu Lys Met
145             150             155             160
Asn Leu Lys Asp Pro Asn Ser Pro Asn Leu Asp Thr Leu Val Asp Gln
      165             170             175
Ser Ser Gly Ser Val Trp Phe Asn Phe Tyr Glu Pro Glu Ser Asn Arg
      180             185             190
Val Val His Asp Phe Ala Val Glu Val Gly Thr Phe Gln Ala Ile Thr
      195             200             205
Tyr Thr Tyr Thr Ser Thr Asn Asn Ala Ser Gly Gly Phe Asn Ser Ser
      210             215             220
Lys Ser Val Ile His Glu Asn Leu Asp Lys Asn Arg Glu Asp Ala Ile
225             230             235             240
His Lys Ile Leu Asn Arg Met Tyr Ala Val Met Lys Lys Ala Val
      245             250             255
Thr Glu Leu Thr Lys Glu Asn Ile Ala Lys Tyr Arg Asp Ala Ile Asp
      260             265             270
Arg Met Lys Gly Phe Lys Ser Ser Met Pro Gln Lys Lys
      275             280             285

```

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803

```

Glu Leu Val Leu Phe Glu Lys Leu Lys Phe Phe Lys Ile Lys Lys Asp
1              5              10              15
Asp Glu Asn Gln Pro Glu Val Asn Leu Asn Ser Glu Ile Tyr Glu Gln
      20              25              30
Phe Lys Val Phe Arg Leu Pro Leu Ile Leu Ile Gln Leu Leu Val Leu
      35              40              45
Leu Gly Thr Leu Gly Tyr Phe Ala Leu Glu Asn Tyr Ser Leu Met Gln
      50              55              60
Ala Phe Phe Gln Thr Thr Tyr Thr Met Thr Ala Thr Gly Phe Gly Ala
65              70              75              80
Leu Asn Glu Ser Gln Phe Gly Pro Ile Ser Ile Phe Leu Thr Ser Ile
      85              90              95
Leu Met Phe Cys Gly Thr Gly Ile Ile Ala Phe Ser Val Ala Ile Leu
      100             105             110

```

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```

Val Ser Val Val Asn Lys Gly Thr Leu Thr Arg Leu Ile Lys Glu Lys
      115      120      125
Gly Met Ile Tyr Lys Ile Ala Arg Leu Lys Asp His Tyr Val Ile Cys
      130      135      140
Tyr His Asn Glu Tyr Thr Ile Glu Leu Ser Lys Gln Phe Arg Ser Ala
145      150      155      160
Gln Ile Pro Phe Val Val Val Asp Asn Asp Pro Asn Phe Glu Glu Glu
      165      170      175
Ala Ile Lys His Lys Tyr Pro Tyr Tyr Ile Ile Gly Asp Pro His Thr
      180      185      190
Asn Leu Ala Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val
      195      200      205
Ala Leu Ser Lys Ile Leu Pro Val Asn Val Ala Leu Met Val Ser Val
210      215      220
Arg Leu Phe Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala
225      230      235      240
Ser Ala His Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Leu Gly Ala
      245      250      255
Asp Met Val Val Ser Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala
260      265      270
Met Ala Val Arg Pro Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn
275      280      285
Lys Lys Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr
290      295      300
Ser Trp Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile
305      310      315      320
Ala Lys Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile
      325      330      335
Pro Met Pro Asp Gly Lys Arg Leu Leu Gln Ala Asn Pro Ser Tyr
340      345      350

```

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804

```

Thr Lys Lys Leu Asn Asn Thr Leu Phe Asn Lys Gly Leu Ile Ile Phe
1      5      10      15
Lys Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly
      20      25      30
Phe Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr
35      40      45
Pro Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile
50      55      60
Ile Asn Arg Gln Lys Leu Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu
65      70      75      80
Gly Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu
      85      90      95
Met Lys Asp Trp Met Pro Arg Ser Ile

```

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(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805

```

Ile Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile
1           5           10           15
Phe Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly
          20           25           30
Tyr Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu
          35           40           45
Ser Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys
          50           55           60
Lys Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys
65           70           75           80
Lys Ala Cys Glu Glu Val Phe
          85

```

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806

```

Arg Ala Ile Thr Thr Asn Gln Phe Val Gly Thr Asn Met Phe Phe Lys
1           5           10           15
Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala Leu Tyr Leu Val
          20           25           30
Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val Glu Met Ile Ala
          35           40           45
Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala Asp Ser Ile Thr
50           55           60

```

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```

Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala Val Asn Phe Val
65          70          75          80
Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser Gln Val Thr Pro
      85          90          95
Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr Tyr Lys Ile Phe
      100        105        110
Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys Ile Ser Gln Leu
      115        120        125
Glu Gln Lys Gly Val Met Met Glu Pro Gln Thr Leu Asn Phe Gly Glu
      130        135        140
Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile Glu Ala Glu Ile
145          150          155          160
Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp Lys
      165          170

```

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807

```

Ile Ser Asn Met Glu Asn Thr Pro Lys Asp Arg Ala Arg Ile Leu Ile
1          5          10          15
Glu Glu Leu Lys Ile Leu Gln Gly Val Ile Asn Arg Met Ala Gln Asn
      20          25          30
Ser Leu Glu Cys Lys Lys Trp Thr Leu Ala Leu Ala Val Gly Val Leu
      35          40          45
Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly Leu Cys Val Leu
      50          55          60
Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala Tyr Tyr Leu Met
65          70          75          80
Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu Ile Lys Asn Arg
      85          90          95
Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro Ile His Gln Thr
      100        105        110
Cys Gln Ser Thr Gln Phe Leu Ser Ala Met Arg Ser Phe Ser Leu Phe
      115        120        125
Pro Tyr Trp Ala Leu Gly Leu Cys Leu Val Gly Tyr Gly Phe Cys Cys
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808

```

Pro Leu Lys Ser Lys Ala Ser Lys Leu Leu Gly Ala Asn Ile Val Tyr
1      5      10      15
Lys Ile His Cys Leu Val Lys Gly Val Thr Leu Glu Gln Gln Asn Lys
20      25      30
Leu Leu Lys Thr Ile Glu Pro Phe Lys Lys Phe Ala Ser Leu Glu Phe
35      40      45
Ile Asp Ile Asn Ser Leu Asp Tyr Ser Ile Glu Ser Tyr Leu Asn Glu
50      55      60
Ser Cys Ser Lys Arg Tyr Gly Gly Leu Leu Val Leu Cys Arg Leu Leu
65      70      75      80
Leu Ala Ser Leu Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp Val
85      90      95
Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu Asp
100     105     110
Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser His
115     120     125
Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys Asn
130     135     140
Phe Lys Ile Asp Leu Leu Arg Phe Ser Gln Asn Glu Leu Lys Arg Ile
145     150     155     160
His Gln Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu Trp
165     170     175
Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr Arg
180     185     190
Gly Lys Asp Leu Phe Tyr Pro Glu Gln Cys Leu Ile Asn Met Val Phe
195     200     205
Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser Asp
210     215     220
Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe Ile
225     230     235     240
Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu Ile
245     250     255
Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys Thr
260     265     270
Pro Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys Asp
275     280     285
Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile Arg
290     295     300
Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe Glu
305     310     315     320
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809

```

Lys Lys Phe Ser Asn Ser Leu Lys Gly Gln Lys Lys Thr Met Lys Phe
1      5      10      15
Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys Phe Leu Met
20      25      30
Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn Ser Asp Leu
35      40      45
Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile Gly Phe Val
50      55      60
Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu Lys Tyr Ser
65      70      75      80
Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser Val Ala Glu
85      90      95
Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys Gly Leu Ile
100     105     110
Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala Phe Ile Lys
115     120     125
Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu Ile Ala Leu
130     135     140
Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val Pro Gly Val
145     150     155     160
Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly Ser Val Arg
165     170     175
Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys Arg Ser Leu
180     185     190
Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr Leu Ser Leu
195     200     205
Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu Asn Asn Leu
210     215     220
Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile Ser Asn Val
225     230     235     240
Val Leu Val Ile Gly Glu Ser Ala Ser Arg Asn Phe Met Gln Leu Tyr
245     250     255
Gly Tyr Ser Val Pro Asn Asn Pro Leu Cys Glu Arg Thr Arg Gln Ala
260     265     270
Arg Glu Arg Glu Arg Glu Ser Asn Asn Leu Phe Val Phe Ser Asp Thr
275     280     285
Ile Ser Lys Glu Ala His Thr Ser Asp Val Phe Glu Ser Leu Leu Asn
290     295     300
Tyr Ser Asp Ala Glu Thr Thr Lys Pro Trp Tyr His Tyr His Asn Met
305     310     315     320
Ile Asp Ile Phe Lys Arg Ser His Tyr Glu Thr Phe Trp Leu Glu Lys
325     330     335
Gln Ile Val Asp Glu Trp Gly Ile Thr Gln Asn Leu Val Ser Asn Arg
340     345     350
Ser Lys Asn Arg Tyr Tyr Ile Leu Gly Asn Tyr Gly Ala Tyr Asp Glu
355     360     365
Glu Leu Val Lys Phe Tyr Ser Lys Asn Val Gln Pro Gln Leu Lys Ser
370     375     380
Lys Asn Phe Ile Val Phe His Leu Leu Gly Ser His Ser Trp Tyr Ala
385     390     395     400
Asp Arg Phe Pro Lys Ser Phe Ala Lys Phe Lys Pro Ser Asp Leu Ser
405     410     415
Phe Ser Asn Leu His Ala Ser Ser Asp Arg Asp Lys Gln Ile Val Ala
420     425     430
Asp Tyr Val Asn Ser Leu Tyr Tyr Asn Asp Phe Val Leu Asn Gly Ile

```

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```

      435              440              445
Phe Asn Leu Phe Lys Asp Lys Asp Ala Ile Val Phe Tyr Leu Ser Asp
  450              455              460
His Ala Gln Asp Ile Phe Glu Ser Gly Pro Thr Tyr Gly His Ser Cys
  465              470              475              480
Ser Lys Ala Gly Leu Glu Ile Pro Phe Met Ile Tyr Val Ser Asp Ile
      485              490              495
Phe Lys Glu Lys His Pro Glu Lys Val Lys Leu Ile Lys Asn Ala Leu
      500              505              510
Asn Lys Pro Phe Met Ser Asp Asp Leu Ile His Ser Leu Leu Pro Leu
      515              520              525
Val Gly Ile His Thr Lys Asp Glu Ile Glu Ser Lys Asn Leu Phe Ser
      530              535              540
Pro Gln Phe Asp Ala Gln Arg Lys Arg Ala Val Cys Tyr Gly Ser Met
  545              550              555              560
Asn Tyr Asp Arg Thr Lys
      565

```

(2) INFORMATION FOR SEQ ID NO:1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810

```

Lys Ser Phe Met Pro Pro Thr Arg Pro Gln Ala Ser Ile Leu Arg Leu
  1              5              10              15
Thr Leu Lys Asn Pro Leu Ser Met Leu Ser Arg Tyr Ser Leu Cys Leu
      20              25              30
Leu Lys Lys Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala
      35              40              45
Cys Leu Ile Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn
      50              55              60
Thr Leu Lys Ile Arg Ser Leu Leu Lys Pro
  65              70

```

(2) INFORMATION FOR SEQ ID NO:1811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811

```

Thr Ser Ala Ser Arg Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn
1          5          10          15
Leu Cys Ala Arg Lys Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn
          20          25          30
Glu Met Leu Ile Arg Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu
          35          40          45
Leu Asp Glu Ala Ile Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val
          50          55          60
Gln Asp Glu Asn Ala Leu Gln Pro Phe Glu Gln Ser Phe Gln Gln Leu
65          70          75          80
Glu Glu Ile Leu Arg
          85

```

(2) INFORMATION FOR SEQ ID NO:1812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812

```

Asp Lys Arg Asn Ile Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu
1          5          10          15
Thr Tyr Lys Ile Thr Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly
          20          25          30
Leu Val Val Gly Leu Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile
          35          40          45
Asn Glu Met Thr Leu Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly
          50          55          60
Val Leu Ile Leu Thr Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr
65          70          75          80
Thr Lys Thr Leu Ile Lys Leu Ile Pro Lys Ile Ile Gly
          85          90

```

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813

```

Lys Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys
1      5      10      15
Ile Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile
20      25      30
Ser Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala
35      40      45
Pro Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile
50      55      60
Cys Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser
65      70      75      80
Lys Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe
85      90      95
Leu Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala
100     105     110
Gly Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val
115     120     125
Asn Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser
130     135     140
Ser Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His
145     150     155     160
Gly Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser
165     170     175
His Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn
180     185     190
Asp Tyr Ala Gly Gln Ala Phe Arg Gly Arg Gly Leu Lys Gly Leu Leu
195     200     205
Ser Lys Lys Ser Gly Ala Leu Pro Lys Gln His Ala Asn Phe Leu Val
210     215     220
Asn Leu Gly Gly Ala Glu Phe Glu Glu Ala Leu Asp Leu Ile Glu Leu
225     230     235     240
Ala Lys Thr Arg Val Leu Gln Glu Tyr Gly Ile His Leu Glu Glu Glu
245     250     255
Val Lys Ile Leu Arg
260

```

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814

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```

Leu Asn Ser Glu His Pro Leu Phe Asp Trp Ala Ser Lys Gln Thr Tyr
1      5      10      15
Ile Gln Met Ala Asn Met Met Met Ala Ala Met Leu Gly Ile Asp
20      25      30
Ser Cys Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Ala Ala Tyr Leu
35      40      45
Glu Glu Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met
50      55      60
Ala Ser Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp
65      70      75      80
Lys Thr Glu Val Ile Tyr Glu Val Ile Glu
85      90

```

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815

```

Lys Glu Ile Thr Met Arg Lys Leu Phe Ile Pro Leu Leu Leu Phe Ser
1      5      10      15
Ala Leu Glu Ala Asn Glu Lys Asn Gly Phe Phe Ile Glu Ala Gly Phe
20      25      30
Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Gln Glu Lys Arg His Thr
35      40      45
Thr Thr Lys Asn Thr Tyr Ala Thr Tyr Asn Tyr Leu Pro Thr Asp Thr
50      55      60
Ile Leu Lys Arg Ala Ala Asn Leu Phe Thr Asn Ala Glu Ala Ile Ser
65      70      75      80
Lys Leu Lys Phe Ser Ser Leu Ser Pro Val Arg Val Leu Tyr Met Tyr
85      90      95
Asn Gly Gln Leu Thr Ile Glu Asn Phe Leu Pro Tyr Asn Leu Asn Asn
100      105      110
Val Lys Leu Ser Phe Thr Asp Ala Gln Gly Asn Val Ile Asp Leu Gly
115      120      125
Val Ile Glu Thr Ile Pro Lys His Ser Lys Ile Val Leu Pro Gly Glu
130      135      140
Ala Phe Asp Ser Leu Lys Ile Asp Pro Tyr Thr Leu Phe Leu Pro Lys
145      150      155      160
Ile Glu Ala Thr Ser Thr Ser Ile Ser Asp Ala Asn Thr Gln Arg Val
165      170      175
Phe Glu Thr Leu Asn Lys Ile Lys Thr Asn Leu Val Val Asn Tyr Arg
180      185      190
Asn Glu Asn Lys Phe Lys Asp His Glu Asn His Trp Glu Ala Phe Thr
195      200      205
Pro Gln Thr Ala Glu Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala
210      215      220
Val Leu Asp Ser Gln Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe
225      230      235      240
Glu Phe Thr Asn Ser Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys

```

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```

                245                250                255
Val Asn Pro Gly Thr Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys
                260                265                270
Tyr Val Leu Asn Lys Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala
                275                280                285
Asp Leu Asp Val Ile Val Leu Lys Asp Ser Gly Val Val Gly Leu Gly
                290                295                300
Ser Asp Ile Thr Pro Ser Asn Asn Asp Asp Gly Lys His Tyr Gly Gln
                305                310                315                320
Leu Gly Val Val Ala Ser Ala Leu Asp Pro Lys Lys Leu Phe Gly Asn
                325                330                335
Asp Leu Lys Thr Ile Asn Leu Glu Asp Leu Arg Thr Ile Leu His Glu
                340                345                350
Phe Ser His Thr Lys Gly Tyr Gly His Asn Gly Asn Met Thr Tyr Gln
                355                360                365
Arg Val Pro Val Thr Lys Asp Val Lys
                370                375

```

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816

```

Ile Met Gly Val Gly Glu Lys Glu Glu Lys Lys Glu Ser Gln Lys Val
1      5      10      15
Ala Val Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Glu Cys Val Leu
20     25     30
Met Leu Leu Asn Gln Gly Tyr Lys Val Tyr Ala Leu Ser Arg His Ala
35     40     45
Thr Leu Cys Val Ala Leu Asn His Ala Leu Cys Glu Cys Val Asp Ile
50     55     60
Asp Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser
65     70     75     80
Ala Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly
85     90     95
Val Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln
100    105    110
Phe Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu
115    120    125
Pro Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser
130    135    140
Ile Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser
145    150    155    160
Lys His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys
165    170    175
Pro Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser
180    185    190
Asn Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val
195    200    205

```

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Tyr Ala Leu Glu Val Asn Ala Ala
210 215

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817

```

Asp Ser Asn Arg Ser Ala Phe Ile Cys His Asn Leu Ala Met Val Leu
1      5      10      15
Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val Leu Ser Glu
20      25      30
Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp Val Ala Asp
35      40      45
Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu Lys Lys Lys
50      55      60
Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn Lys Ile Ala
65      70      75      80
Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr Ile Leu Ser
85      90      95
Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro Lys Asp Leu
100     105     110
Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys Asp Ile Val
115     120     125
Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr Ala Leu Ile
130     135     140
Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp Phe Thr Phe
145     150     155     160
Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val Thr Phe Asn
165     170     175
Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe Leu Asn His
180     185     190
Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala Leu Glu Trp
195     200     205
Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro Lys Glu Ala
210     215     220
Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu Thr Gly Cys
225     230     235     240
Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys Lys Gly Arg
245     250     255

```

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...196
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818

```

Gly Asn Ala Arg Thr Cys Ile Val Ile Cys Trp Asp Cys Leu Asn Gln
1      5      10      15
Gln Trp Asp Cys Gly Leu Thr Lys Val Asp Pro Lys Ser Thr Ala Val
20      25      30
Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val Val
35      40      45
Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala Glu
50      55      60
Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro Ala
65      70      75      80
Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn His
85      90      95
Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe Val
100     105     110
Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp Met
115     120     125
Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp Ala
130     135     140
Ile Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Ala Phe Ile Glu
145     150     155     160
Asn Ile Leu Lys Ile Pro Leu Gly Lys Phe Thr Pro Trp Leu Ala Ile
165     170     175
Ile Glu Gly Ile Leu Thr Ala Trp Ile Pro Ala Trp Leu Leu Phe Ile
180     185     190
Gln His Trp Val
195

```

(2) INFORMATION FOR SEQ ID NO:1819:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 640 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...640
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819

```

Ser Ile Cys His Glu Tyr Leu Lys Val Asn Leu Gln Glu Lys Leu Ala
1      5      10      15
Gly Phe Arg Asp Phe Val His Tyr Asn Glu Asn Ala Lys Asp Ser Leu
20      25      30

```

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Pro Leu Lys Ala Leu Phe Leu Ser Gly Val Asp Ala Leu Ser Lys Asp
 35 40 45
 Ala Leu Tyr Tyr Leu Glu Lys Ile Met Arg Phe Gly Ser Lys Asn Gly
 50 55 60
 Val Leu Ser Phe Val Asn Leu Glu Ser Glu Lys Asn Asn Gln Ser Ala
 65 70 75 80
 Glu Asp Leu Lys Arg Tyr Ala Glu Phe Phe Lys Asp Arg Thr Ser Phe
 85 90 95
 Glu Gly Leu Lys Tyr Leu Asn Val Glu Ile Ile Ser Asp Gln Gly Ile
 100 105 110
 Lys Ser Gln His Met Gln Asp Phe Ala Asp Lys Ile Lys Ala Tyr Tyr
 115 120 125
 Lys Gln Lys Lys Glu Val Lys Arg Glu Leu Lys Asp Leu Gln Arg Asp
 130 135 140
 Lys Glu Phe Trp Thr Lys Ser Ser Gln His Glu Val Ser Val Pro Val
 145 150 155 160
 Gly Trp Asp Ile Asn His Lys Glu Val Cys Phe Lys Ile Gly Asn Glu
 165 170 175
 Gln Asn His Thr Leu Ile Cys Asp His Ser Gly Ser Gly Lys Ser Asn
 180 185 190
 Phe Leu His Val Leu Ile Gln Asn Leu Ala Phe Tyr Tyr Asp Pro Asp
 195 200 205
 Glu Val Gln Leu Phe Leu Leu Asp Tyr Lys Glu Gly Val Glu Phe Asn
 210 215 220
 Ala Tyr Val Ala Asp Pro Ala Leu Glu His Ala Arg Leu Val Ser Val
 225 230 235 240
 Ala Ser Ser Ile Ser Tyr Gly Ile Thr Phe Leu Lys Trp Leu Cys Asp
 245 250 255
 Glu Met Gln Lys Arg Ala Asp Arg Phe Lys Gln Phe Asn Val Lys Asp
 260 265 270
 Leu Ser Asp Tyr Arg Lys His Glu Lys Met Pro Arg Leu Ile Val Val
 275 280 285
 Ile Asp Glu Phe Gln Val Leu Phe Ser Asp Asn Lys Ser Thr Lys Ala
 290 295 300
 Val Glu Gly His Leu Asn Thr Leu Leu Lys Lys Gly Arg Ser Tyr Gly
 305 310 315 320
 Val His Leu Val Leu Ala Thr Gln Thr Met Arg Gly Thr Asp Ile Asn
 325 330 335
 Pro Ser Phe Lys Ala Gln Ile Ala Asn Arg Ile Ala Leu Pro Met Asp
 340 345 350
 Ala Glu Asp Ser Ser Ser Val Leu Gly Asp Asp Ala Ala Cys Glu Ile
 355 360 365
 Gln Asn Pro Glu Gly Ile Phe Asn Asn Asn Gly Gly Asn Arg Lys Tyr
 370 375 380
 His Thr Lys Met Ser Val Pro Lys Ala Pro Asp Asp Phe Lys Ser Phe
 385 390 395 400
 Leu Thr Lys Ile His Ala Glu Phe Asn Gln Arg Asn Leu Ala Pro Ile
 405 410 415
 Asp Arg Lys Ile Tyr Asn Gly Glu Thr Pro Leu Lys Met Pro Asp Thr
 420 425 430
 Leu Lys Ala Asn Glu Met Arg Leu His Leu Gly Lys Lys Val Asp Tyr
 435 440 445
 Glu Gln Lys Asp Leu Ile Val Glu Phe Glu Ser Asn Glu Ser His Leu
 450 455 460
 Leu Val Val Ile Gln Asp Leu Asn Ala Arg Ile Ala Leu Met Lys Leu
 465 470 475 480
 Leu Phe Gln Asn Val Lys Ser Ala Asn Lys Glu Leu Val Phe Cys Asn
 485 490 495
 Lys Glu Lys Arg Leu Ile Arg Ser Phe Asp Ala Gln Lys Glu Tyr Gly
 500 505 510
 Ile Thr Pro Val Glu Asn Ile Leu Ser Val Leu Asp Thr Ala Met Asn
 515 520 525
 Pro Asn Ser Ala Leu Val Ile Asp Asn Leu Asn Glu Ala Lys Glu Leu
 530 535 540
 His Asp Lys Val Gly Ala Glu Lys Leu Lys Ser Phe Leu Glu Lys Ala

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```

545          550          555          560
Ile Asp Asn Glu Gln Tyr Cys Val Ile Phe Ala His Asp Phe Arg Gln
          565          570          575
Ile Lys Thr Asn Tyr His Phe Asp Lys Leu Lys Glu Leu Leu Asn Asn
          580          585          590
His Phe Lys Gln Cys Leu Ala Phe Arg Cys Asn Gly Glu Asn Leu Asn
          595          600          605
Ala Ile Lys Ser Asp Leu Pro Pro Ser Lys Leu Asn Val Leu Leu
          610          615          620
Ile Glu Leu Ser Lys Asp Ser Val Thr Glu Phe Arg Pro Phe Ser Leu
625          630          635          640

```

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820

```

Arg Pro Asn Leu Ser Ser Gln Phe Leu Tyr Thr Glu Met Leu Ser Leu
1          5          10          15
Lys Leu Thr Tyr Glu Ser Thr Leu Gln Gln Asp Leu Lys Lys Ile Leu
          20          25          30
Gly Ile Glu Glu Val Ile Met Leu Ser Thr Ser Pro Met Glu Leu Arg
          35          40          45
Leu Ala Asn Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala
          50          55          60
Met Asn Glu Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr
65          70          75          80
Thr Gln Arg Ser His Pro Cys His
          85

```

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821

```

Glu Lys Ser Thr Ser Asn Leu Lys Lys Pro Ser Val Trp Arg Ser Lys
1      5      10      15
Leu Ile Cys Lys Ile Ala Thr His Lys Ala Arg Ser Ile Gly Leu Cys
      20      25      30
Val Lys Pro Lys Ser Met Lys Glu Lys Leu Arg Gly Ala Met Val Asn
      35      40      45
Ile Leu Arg Ile Lys Met Ile Glu Ile Ser Glu Trp Leu Gln Lys Leu
      50      55      60
Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe
65      70      75      80
Leu Lys Pro Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg
      85      90      95
Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Gly
      100      105      110
Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
      115      120      125
Asn Gly Ala Asn Met Glu Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro
130      135      140
Pro Lys Ser Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg
145      150      155      160
Glu Met Leu Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu
      165      170      175
Val Ile Leu Ile Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala
      180      185      190
Arg Arg Leu Leu Asp Lys Asn Asn Asp Phe Ile Tyr Gln Gln Arg Ile
195      200      205
Leu Thr Glu Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Pro
210      215      220

```

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822

```

Thr Trp Val His Phe Leu Thr Leu Thr Leu Lys Gln Pro Lys Asp Pro
1      5      10      15
Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met Glu
      20      25      30
Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met
      35      40      45
Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln
      50      55      60
Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys
65      70      75      80
Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln Asn
      85      90      95
Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met

```

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Ser 100 105 110

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823

```

Arg Ala Ser Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Lys Leu
1          5          10          15
Lys Lys Arg His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala
20          25          30
Asn Gly Phe Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly
35          40          45
Ser Ala Tyr Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn
50          55          60
Pro Ala Asn Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu
65          70          75          80
Phe Glu Met Thr Thr Thr Val Ile Asn Ile Pro Ala Phe Ser Phe Lys
85          90          95
Val Pro Thr Thr Asn Gln Gly Leu Tyr Ser Val Thr Ser Leu Glu Ile
100         105         110
Asp Lys Ser Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu
115         120         125
Gly Asn Ile Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu
130         135         140
Ser Gln Gly Ile Asn Arg Val Gln Gly Val Met Asn
145         150         155

```

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...217

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824

```

Ala Asp Arg Glu Asp Lys Leu Ser His Ser Ile Ile Met Arg Tyr Phe
1      5      10      15
Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe Phe Val Ser Cys
      20      25      30
Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr Lys Glu Arg Ile
      35      40      45
Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr Leu Asn Ala Leu
      50      55      60
Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val Phe Arg Phe Tyr
      65      70      75      80
Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn Thr Glu Val Thr
      85      90      95
Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr Met Thr Lys Arg
      100      105      110
Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp Ile Ala Ala Arg
      115      120      125
Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe Asp Asp Ile Val
      130      135      140
Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg His Leu Thr Pro
      145      150      155      160
Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu Ile Ile Leu Tyr
      165      170      175
Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu Thr Gln Lys Ile
      180      185      190
Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln Asp Leu Glu Asp
      195      200      205
Asn Glu Asn Ala Asp Ser Glu Leu Gln
      210      215

```

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825

```

Glu Ile Ala Glu Ile Val Ser Gln Trp Thr His Ile Pro Phe Gln Lys
1      5      10      15
Met Phe Gln Ser Glu Lys Asn Arg Val Leu Asn Ile Glu Ser Glu Leu
      20      25      30
Gln Lys Arg Val Val Gly Gln Glu Lys Ala Leu Lys Ala Ile Ala Lys
      35      40      45
Ala Ile Lys Arg Asn Lys Ala Gly Leu Ser Asp Ser Asn Lys Pro Ile
      50      55      60
Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Ser
      65      70      75      80
Ala Lys Ala Leu Ala Gln Phe Leu Phe Asp Ser Asp Lys Asn Leu Ile
      85      90      95
Arg Ile Asp Met Ser Glu Tyr Met Glu Lys His Ala Ile Ser Arg Leu

```

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```

      100      105      110
Ile Gly Ala Ala Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu
      115      120      125
Thr Glu Ala Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu
      130      135      140
Val Glu Lys Ala His Pro Asp Val Phe Asn Phe Leu Leu Gln Val Phe
      145      150      155      160
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
      165      170      175
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
      180      185      190
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
      195      200      205
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
      210      215      220
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826

```

Val Arg Phe Cys Tyr Ser Lys Lys Tyr Lys Lys Thr Ile Ile Leu Lys
1      5      10      15
Lys Asp Trp Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Glu Thr
      20      25      30
Ala Pro Leu Leu Thr Ser Leu Leu Ala Gly Ile Leu Thr Phe Leu Ser
      35      40      45
Pro Cys Val Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln
      50      55      60
Ile Ser Leu Glu Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val
      65      70      75      80
Phe Leu Lys Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu
      85      90      95
Gly Val Gly Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser
      100      105      110
Trp Val Asn Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His
      115      120      125
Phe Leu Gly Val Phe Arg Phe Ala Leu Leu Tyr Lys Thr Gln Ser Ala
      130      135      140
Gly Leu Ala Ser Lys Ser Asn Ser Met Gln Arg Phe Tyr Pro Phe Leu
      145      150      155      160
Leu Gly Met Ser Phe Ala Leu Gly Trp Thr Pro Cys Ile Gly Pro Ile
      165      170      175
Phe Thr Ser Ile Val Ile Met Ser Ala Ser Lys Asp Ala Tyr Gly Leu
      180      185      190
Met Leu Met Val Val Phe Val Met Gly Leu Ala Ile Pro Phe Val Leu
      195      200      205

```

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```

Val Ala Leu Met Leu Glu Arg Ala Leu Leu Phe Leu Lys Ser Leu Arg
 210                215                220
Lys Tyr Asn Arg Ala Ile Glu Ile Val Ser Gly Leu Val Leu Ile Leu
 225                230                235                240
Met Gly Ile Leu Ile Met Thr Asn Ser Leu Glu Ser Leu Thr Asn Phe
                245                250                255
Leu Gln Asn

```

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827

```

Ile Gly Gly Ala His Ala Phe Leu Tyr Tyr Leu Thr Phe Leu Phe Ile
 1                5                10                15
Val Gly Phe Gly Val Phe Val Tyr Ser Ile Asp Pro Gln Ala Tyr Ala
 20                25                30
Phe Asn Leu Gly Ser Tyr Ser Phe Asn Leu Pro Ile Ala Val Trp Leu
 35                40                45
Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
 50                55                60
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
 65                70                75                80
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
 85                90                95
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
 100               105               110
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
 115               120               125
Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
 130               135               140
Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
 145               150               155               160
Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
 165               170               175
Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
 180               185               190
Leu Arg Arg Tyr Ala Leu
 195

```

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828

```

Gln Asp Lys Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn
1      5      10      15
Ala Ser Gln Asn Ile Leu Ser Leu Ser Val Leu His Asn Gln Ile
20      25      30
Lys Met Ser Tyr Gly Asn Lys Val Met Asp Phe Thr Pro Pro Thr Leu
35      40      45
Gln Asp Tyr Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile
50      55      60
Glu Ala Val Gly Gly Asn Asn Ala Ile Lys Trp Leu Ser Thr Leu Met
65      70      75      80
Met Glu Thr Lys Glu Asn Pro Leu Phe Ala Pro Ile Tyr Leu Glu Asn
85      90      95
His Ser Leu Asn Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr
100      105      110
Ala Ser Leu Ile Ser Asn Pro Asn Phe Arg Asn Asn Ala Thr Ser Leu
115      120      125
Leu Glu Met Ala Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu
130      135      140
Ser Asp Phe Arg Ala Arg Glu Gly Glu Ser Asn Phe Ser Glu Arg Leu
145      150      155      160
Leu Glu Leu Lys Asn Lys Arg Phe Ser Asp Pro Asn Pro Ser Glu Val
165      170      175
Phe Val Lys Tyr Ser Gln Leu Ser Lys His Pro Asn Asn Leu Trp Ile
180      185      190
Gln Gly Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu
195      200      205
Tyr Gly Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu
210      215      220
Gly Gly Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met
225      230      235      240
His Ser Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe
245      250      255
Leu Lys Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly
260      265      270
Asn Ala Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn
275      280      285
Gln Arg Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr
290      295      300
Gly Tyr Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln
305      310      315      320
Val Gly Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys
325      330      335
Met Gln Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser
340      345      350
Asn Glu Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr
355      360      365
Phe Gly Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp
370      375      380
Leu Leu Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu
385      390      395      400
Asn Thr Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser
405      410      415

```

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Val Ile Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn
 420 425 430
 Ala Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile
 435 440 445
 Thr Gly Asn Val Gly Met Arg Val Ala Phe
 450 455

(2) INFORMATION FOR SEQ ID NO:1829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829

Thr Ile Leu Cys Pro Gly Ala Lys Ser Tyr Lys Tyr Trp Glu Gly Met
 1 5 10 15
 Gly Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr Thr
 20 25 30
 Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn Leu
 35 40 45
 Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr Leu
 50 55 60
 Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Lys Pro Val Gly Thr
 65 70 75 80
 Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Asp Glu Lys Ile Ile Leu
 85 90 95
 Val Lys Asn Gln Asp Tyr Trp Gly Leu Lys Ala Tyr Leu Asp Lys Val
 100 105 110
 Val Val Arg Thr Ile His Asn Phe Ser Thr Arg Ala Leu Ala Leu Arg
 115 120 125
 Thr Gly Glu Ile Met Leu Met Thr Gly His Asn Leu Asn Glu Val Glu
 130 135 140
 Gln Leu Glu Lys Leu His Asn Ile Val Val Asp Arg Ser Pro Gly Leu
 145 150 155 160
 Ile Ala Asn Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr Phe Asn Asn
 165 170 175
 Pro Leu Val Arg Leu Ala Ile Asn His Ala Ile Asn Val Asp Asp Tyr
 180 185 190
 Ile Lys Val Ile Tyr Glu Gly Phe Ala Gln Lys Met Val Asn Pro Phe
 195 200 205
 Pro Pro Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro Tyr Glu Tyr
 210 215 220
 Asp Leu Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly Tyr Pro Asn
 225 230 235 240
 Gly Phe Lys Thr Asn Ile Cys Thr Ser Leu Leu
 245 250

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 879 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830

```

Ile His Ile Lys Arg Ile Phe Leu Leu Lys Asn Thr Pro Phe Asn Pro
1          5          10          15
Pro Leu Phe Leu His Ile Ala Pro Leu Lys Pro Phe Met Ile Ile Ile
20          25          30
Asn Leu Phe Trp Asn Thr Phe Ser Leu Phe Val Lys Lys Thr Asn Lys
35          40          45
Asp Leu Ile Met Arg Val Thr Phe Gly Ser Lys Tyr Asn Gln Met Asn
50          55          60
His Tyr Gln Asn Ala Leu Gln Asn Lys Ile Asn Asp Ala Asn Thr Gln
65          70          75          80
Ile Ala Ser Gly Leu Lys Ile Arg Tyr Gly Tyr Gln Asn Ser Asp Ile
85          90          95
Asn Asn Gln Asn Leu Lys Phe Gln Tyr Glu Glu Asn Thr Leu Asp Gln
100         105         110
Gly Ile Asp Val Ala Gln Asn Ala Tyr Thr Ser Thr Leu Asn Thr Asp
115         120         125
Lys Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys
130         135         140
Leu Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala
145         150         155         160
Ile Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala
165         170         175
Asn Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp
180         185         190
Arg Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp
195         200         205
Leu Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser
210         215         220
Gly Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile
225         230         235         240
Thr Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu His Pro Asp Val
245         250         255
Met Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys
260         265         270
Pro Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro
275         280         285
Thr Asn Asp Pro Lys Glu Phe Tyr Leu Gln Gly Ile Arg Pro Asp
290         295         300
Gly Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn
305         310         315         320
Gln Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His
325         330         335
Ala Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn
340         345         350
Asn Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn
355         360         365
Leu Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp
370         375         380

```

SUBSTITUTE SHEET (RULE 26)

1357

Ala Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala
 385 390 395 400
 Phe Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met
 405 410 415
 Tyr Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp
 420 425 430
 Asn Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp
 435 440 445
 Lys Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser
 450 455 460
 Ala Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu
 465 470 475 480
 Leu Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys
 485 490 495
 Glu Arg Phe Asn Asn Glu Val Asp Val Glu Ile Glu Thr Asn Gly Arg
 500 505 510
 Leu Arg Ile Ile Asp Asn Ser Ser Lys Glu Ser Pro Ile Ser Phe Ala
 515 520 525
 Leu Ser Thr Leu Asp Gln Lys Gly Leu Glu Val Ala Gly Ile Pro Thr
 530 535 540
 Asn Asn Ala Ser Glu Tyr Gln Lys Thr Tyr Phe Asn Lys Glu Gly Ala
 545 550 555 560
 Lys Leu Glu Ser Asn Val Ala Gln Thr Ala Gln Asn Asp Ala Ala Asn
 565 570 575
 Gly Ser Thr Lys Leu Ser Glu Val Ser Lys Gly Ser Leu Glu Asn Ser
 580 585 590
 Val Phe Asn Met Lys Leu Asn Asp Val Asn Gly Ser Phe Leu Glu Ala
 595 600 605
 Gln Ile Asn Leu Asp Asn Asn Gly Ala Phe Leu Ser Leu Pro Asn Gly
 610 615 620
 Val Lys Ile Pro Leu Tyr Asp Pro Thr Thr Ala Asp Ile Gln Ala Ser
 625 630 635 640
 Lys Pro Asn Glu Val Thr Tyr Arg Gln Leu Met Asp Ala Met Ser Ile
 645 650 655
 Ala Leu Asn Tyr Ser Asn Thr Asp Pro Ala Ile Tyr Gln Gln Ile Ser
 660 665 670
 Asp Asn Pro Thr Ser Lys Glu Ser Lys Glu Arg Phe Ile Glu Leu Leu
 675 680 685
 Lys Gln Ala Lys Asp Asn Leu Ser Ile Asn Leu Asn Glu Glu Gly Lys
 690 695 700
 Val Ile Ile Gln Asp Asn Met His Ser Asn Thr Lys Met Gln Phe Met
 705 710 715 720
 Leu Phe Asp Lys Asp Ala Asn Asp Phe Ser Gln Asn Ala Leu His Ser
 725 730 735
 Asp Lys Pro Ser Leu Lys Leu Asn Ala Asn Asn Ala Leu Ile Asp
 740 745 750
 Lys Pro Ser Val Asn Phe Phe Asp Gln Leu Glu Asn Ile Ile Thr Ser
 755 760 765
 Val Arg Lys Gly Ile Tyr Arg Pro Asp Ala Leu Gly Asp Thr Tyr Ser
 770 775 780
 Ser Asp Met Arg Asn Leu Gly Ile Gln Asn Gly Ile Thr Leu Ile Asp
 785 790 795 800
 His Leu Ser Asp His Ile Glu Lys Met Ile Ala Lys Asn Gly Ala His
 805 810 815
 Gly Lys Ala Phe Glu Asn Ile Ile Arg Arg Asn Glu Val Leu Lys Thr
 820 825 830
 Gln Val Gln Ser Ile Arg Gly Glu Thr Thr Gly Thr Asp Met Ala Glu
 835 840 845
 Thr Tyr Asn Lys Phe Ser Asn Leu Thr Asn Asn Tyr Asn Ala Val Leu
 850 855 860
 Ala Ser Thr Asn Lys Ile Asn Asn Leu Ser Leu Thr Lys Tyr Leu
 865 870 875

(2) INFORMATION FOR SEQ ID NO:1831:

SUBSTITUTE SHEET (RULE 26)

1358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831

```

Arg Ile Asp Gln Ile Lys Ile Met Lys Leu Val Ser Leu Ile Val Ala
1      5      10      15
Leu Val Phe Cys Cys Phe Leu Gly Ala Val Glu Leu Pro Gly Val Tyr
20      25      30
Gln Thr Gln Glu Phe Leu Tyr Met Lys Ser Ser Phe Val Glu Phe Phe
35      40      45
Glu His Asn Gly Lys Phe Tyr Ala Tyr Gly Ile Ser Asp Val Asp Gly
50      55      60
Ser Lys Ala Lys Lys Asp Lys Leu Asn Pro Asn Pro Lys Leu Arg Asn
65      70      75      80
Arg Ser Asp Lys Gly Val Val Phe Leu Ser Asp Leu Ile Lys Val Gly
85      90      95
Glu Gln Ser Tyr Lys Gly Gly Lys Ala Tyr Asn Phe Tyr Asp Gly Lys
100     105     110
Thr Tyr His Val Arg Val Thr Gln Asn Ser Asn Gly Asp Leu Glu Phe
115     120     125
Thr Ser Ser Tyr Asp Lys Trp Gly Tyr Val Gly Asn Thr Phe Thr Leu
130     135     140
Lys Arg Val Arg Gly Ala Glu Ile Ser Ile Leu Lys Leu Lys Arg Phe
145     150     155     160
Asn Leu Met Arg Ser Phe Tyr Arg Gln Thr His Leu Phe Ser Ile Gly
165     170     175
Lys Ala Tyr Ala Thr
180

```

(2) INFORMATION FOR SEQ ID NO:1832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832

SUBSTITUTE SHEET (RULE 26)

1359

```

Lys Asp Leu Ser Lys Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu
1      5      10      15
Ala Ile Ser Leu Cys Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val
20      25      30
Glu Arg Gly Met Ala Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys
35      40      45
Phe Met Cys Asp Ile Val Leu Met Ser Met Gly Val Phe Gly Val Gly
50      55      60
Ala Tyr Phe Ala Lys Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe
65      70      75      80
Gly Ala Val Phe Thr Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu
85      90      95
Phe Gln Thr Phe Lys Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser
100     105     110
Leu Lys Lys Thr Leu Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro
115     120     125
Gln Val Tyr Leu Glu Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser
130     135     140
Phe Asn Leu Val Gln Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala
145     150     155     160
Ala Phe Ser Trp Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly
165     170     175
Ser Lys Leu Leu Asn Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe
180     185     190
Val Thr Ala Ile Met Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe
195     200     205
Leu Ala Leu Leu Ser Lys Thr
210     215

```

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833

```

Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
1      5      10      15
Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
20      25      30
Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
35      40      45
Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp
50      55      60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65      70      75      80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
85      90      95
Glu Asn Leu Ala Glu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
100     105     110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala

```

SUBSTITUTE SHEET (RULE 26)

1360

```

      115      120      125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg
 130      135      140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu
 145      150      155      160
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln
      165      170      175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr
      180      185      190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
      195      200      205
Ile Lys Ser Gly Thr Leu Leu Ala Ser Gly Asn Ala Asn Glu Ile Tyr
      210      215      220
Glu Asn Ala Leu Val Arg Lys Tyr Tyr Leu Gly Glu Asn Phe Lys Val
 225      230      235      240

```

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834

```

Asn Thr Gly Leu Trp His Ser Trp Gly Leu Ala Pro Ala Leu Leu Glu
 1      5      10      15
Thr Gln Leu Pro Lys His Ala His Gln Phe Phe Gln Ile Phe Phe Phe
      20      25      30
Pro Lys Lys Pro Phe Lys Gln Met Ile Val Ile Val Glu Leu Leu Val
      35      40      45
Asn Phe Ile Phe Asn Leu Phe His Ala Ile His Val Gly Val Lys Met
      50      55      60
Ile Asp Asn Ile Lys Leu Pro Leu Arg Arg Ile Lys Met Arg Ala Leu
 65      70      75      80

```

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

1361

(B) LOCATION 1...548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asp | Leu | Gly | Val | Ile | Glu | Thr | Ile | Pro | Lys | His | Ser | Lys | Ile | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Pro | Gly | Glu | Ala | Phe | Asp | Ser | Leu | Lys | Glu | Ala | Phe | Asp | Lys | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Pro | Tyr | Thr | Phe | Phe | Phe | Pro | Lys | Phe | Glu | Ala | Thr | Ser | Thr | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Ser | Asp | Thr | Asn | Thr | Gln | Arg | Val | Phe | Glu | Thr | Leu | Asn | Asn | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Thr | Asn | Leu | Ile | Met | Lys | Tyr | Ser | Asn | Glu | Asn | Pro | Asn | Asn | Phe |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Asn | Thr | Cys | Pro | Tyr | Asn | Asn | Asn | Gly | Asn | Thr | Lys | Asn | Asp | Cys | Trp |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Gln | Asn | Phe | Thr | Pro | Gln | Thr | Ala | Glu | Glu | Phe | Thr | Asn | Leu | Met | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asn | Met | Ile | Ala | Val | Leu | Asp | Ser | Gln | Ser | Trp | Gly | Asp | Ala | Ile | Leu |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Asn | Ala | Pro | Phe | Glu | Phe | Thr | Asn | Ser | Ser | Thr | Asp | Cys | Asp | Ser | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Pro | Ser | Lys | Cys | Val | Asn | Pro | Gly | Val | Asn | Gly | Arg | Val | Asp | Thr | Lys |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Val | Asp | Gln | Gln | Tyr | Ile | Leu | Asn | Lys | Gln | Gly | Ile | Ile | Asn | Asn | Phe |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Arg | Lys | Lys | Ile | Glu | Ile | Asp | Ala | Val | Val | Leu | Lys | Asn | Ser | Gly | Val |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Val | Gly | Leu | Ala | Asn | Gly | Tyr | Gly | Asn | Asp | Gly | Glu | Tyr | Gly | Thr | Leu |
| | 195 | | | | | 200 | | | | | | 205 | | | |
| Gly | Val | Glu | Ala | Tyr | Ala | Leu | Asp | Pro | Lys | Lys | Leu | Phe | Gly | Asn | Asp |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Leu | Lys | Thr | Ile | Asn | Leu | Glu | Asp | Leu | Arg | Thr | Ile | Leu | His | Glu | Phe |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 |
| Ser | His | Thr | Lys | Gly | Tyr | Gly | His | Asn | Gly | Asn | Met | Thr | Tyr | Gln | Arg |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Val | Pro | Val | Thr | Lys | Asp | Gly | Gln | Val | Glu | Lys | Asp | Ser | Asn | Gly | Lys |
| | | 260 | | | | | 265 | | | | | | 270 | | |
| Pro | Lys | Asp | Ser | Asp | Gly | Leu | Pro | Tyr | Asn | Val | Cys | Ser | Leu | Tyr | Gly |
| | | 275 | | | | 280 | | | | | 285 | | | | |
| Gly | Phe | Asn | Gln | Pro | Ala | Phe | Pro | Ser | Asn | Tyr | Pro | Asn | Ser | Ile | Tyr |
| | 290 | | | | 295 | | | | | | 300 | | | | |
| His | Asn | Cys | Ala | Asp | Val | Pro | Ala | Gly | Phe | Leu | Gly | Val | Thr | Ala | Ala |
| 305 | | | | 310 | | | | | | 315 | | | | | 320 |
| Val | Trp | Gln | Gln | Leu | Ile | Asn | Gln | Asn | Ala | Leu | Pro | Ile | Asn | Tyr | Ala |
| | | | 325 | | | | | 330 | | | | | 335 | | |
| Asn | Leu | Gly | Ser | Gln | Thr | Asn | Tyr | Asn | Leu | Asn | Ala | Ser | Leu | Asn | Thr |
| | | 340 | | | | | 345 | | | | | | 350 | | |
| Gln | Asp | Leu | Ala | Asn | Ser | Met | Leu | Ser | Thr | Ile | Gln | Lys | Thr | Phe | Val |
| | 355 | | | | | 360 | | | | | | 365 | | | |
| Thr | Ser | Ser | Val | Thr | Asn | His | Phe | Ser | Asn | Ala | Ser | Gln | Ser | Phe | |
| | 370 | | | | 375 | | | | | | 380 | | | | |
| Arg | Ser | Pro | Ile | Leu | Gly | Val | Asn | Ala | Lys | Ile | Gly | Tyr | Gln | Asn | Tyr |
| 385 | | | | 390 | | | | | | 395 | | | | | 400 |
| Phe | Asn | Asp | Phe | Ile | Gly | Leu | Ala | Tyr | Tyr | Gly | Ile | Ile | Lys | Tyr | Asn |
| | | | 405 | | | | | 410 | | | | | 415 | | |
| Tyr | Ala | Lys | Ala | Val | Asn | Gln | Lys | Val | Gln | Gln | Leu | Ser | Tyr | Gly | Gly |
| | | 420 | | | | | 425 | | | | | | 430 | | |
| Gly | Ile | Asp | Leu | Leu | Leu | Asp | Phe | Ile | Thr | Thr | Tyr | Ser | Asn | Lys | Asn |
| | 435 | | | | | 440 | | | | | | 445 | | | |
| Ser | Pro | Thr | Gly | Ile | Gln | Thr | Lys | Arg | Asn | Phe | Ser | Ser | Ser | Phe | Gly |
| | 450 | | | | 455 | | | | | 460 | | | | | |
| Ile | Phe | Gly | Gly | Leu | Arg | Gly | Leu | Tyr | Asn | Ser | Tyr | Tyr | Val | Leu | Asn |
| 465 | | | | 470 | | | | | | 475 | | | | | 480 |
| Lys | Val | Lys | Gly | Ser | Gly | Asn | Leu | Asp | Val | Ala | Thr | Gly | Leu | Asn | Tyr |

SUBSTITUTE SHEET (RULE 26)

1362

```

          485          490          495
Arg Tyr Lys His Ser Lys Tyr Ser Val Gly Ile Ser Ile Pro Leu Ile
          500          505          510
Gln Arg Lys Ala Ser Val Val Ser Ser Gly Gly Asp Tyr Thr Asn Ser
          515          520          525
Phe Val Phe Asn Glu Gly Ala Ser His Phe Lys Val Phe Phe Asn Tyr
          530          535          540
Gly Trp Val Phe
545

```

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836

```

Asp His Ser Phe Asn Ile Gln Asn Ser Ile Lys Arg Lys Val Met Tyr
1          5          10          15
Ala Ala His Pro Ile Lys Pro Ile Lys Ala Pro Lys Leu Lys Ser Gln
          20          25          30
Phe Leu Arg Arg Val Phe Val Gly Ala Ser Ile Arg Arg Trp Asn Asp
          35          40          45
Gln Ala Cys Pro Leu Glu Phe Val Glu Leu Asp Lys Gln Ala His Lys
          50          55          60
Ala Met Ile Ala Tyr Leu Leu Ala Lys Asp Leu Lys Asp Arg Gly Lys
          65          70          75          80
Asp Leu Asp Leu Asp Leu Ile Lys Tyr Phe Cys Phe Glu Phe Leu
          85          90          95
Glu Arg Leu Val Leu Thr Asp Ile Lys Pro Pro Ile Phe Tyr Ala Leu
          100          105          110
Gln Gln Thr His Ser Lys Glu Leu Ala Ser Tyr Val Ala Gln Ser Leu
          115          120          125
Gln Asp Glu Ile Ser Ala Tyr Phe Ser Leu Glu Glu Leu Lys Glu Tyr
          130          135          140
Leu Ser His Arg Pro Gln Ile Leu Glu Thr Gln Ile Leu Glu Ser Ala
          145          150          155          160
His Phe Tyr Ala Ser Lys Trp Glu Phe Asp Ile Ile Tyr His Phe Asn
          165          170          175
Pro Asn Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln
          180          185          190
Leu His Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu
          195          200          205
Asp Leu Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys
          210          215          220
Arg Trp Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His
          225          230          235          240
Thr Leu Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys
          245          250          255
Ala Cys Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe His
          260          265          270

```

SUBSTITUTE SHEET (RULE 26)

1363

```

Asp Leu Pro Glu Ile Leu Thr Arg Asp Ile Ile Thr Pro Ile Lys Gln
    275                280                285
Ser Val Ala Gly Leu Asp His Cys Ile Lys Glu Ile Glu Lys Lys Glu
    290                295                300
Met Gln Asn Lys Val Tyr Ser Phe Val Ser Leu Gly Val Gln Glu Asp
    305                310                315                320
Leu Lys Tyr Phe Thr Glu Asn Glu Phe Lys Asn Arg Tyr Lys Asp Lys
    325                330                335
Ser His Gln Ile Val Phe Thr Lys Asp Ala Glu Glu Leu Phe Thr Leu
    340                345                350
Tyr Asn Ser Asp Glu Tyr Leu Gly Val Cys Gly Glu Leu Leu Lys Val
    355                360                365
Cys Asp His Leu Ser Ala Phe Leu Glu Ala Gln Ile Ser Leu Ser His
    370                375                380
Gly Ile Ser Ser Tyr Asp Leu Ile Gln Gly Ala Lys Asn Leu Leu Glu
    385                390                395                400
Leu Arg Ser Gln Thr Glu Leu Leu Asp Leu Asp Leu Gly Lys Leu Phe
    405                410                415
Arg Asp Phe Lys
    420

```

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837

```

Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe Lys
1           5           10           15
Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala Leu
    20           25           30
Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu
    35           40           45
Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu
    50           55           60
Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala
    65           70           75           80
Lys Glu Tyr Glu Asn Lys Phe Lys Asn Gln Thr Thr Leu Lys Val Glu
    85           90           95
Glu Ile Leu Gln Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser
    100          105          110
Asp Lys Asp Asp Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
    115          120          125
Val Ala Met Asn Gly Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr
    130          135          140
Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp
    145          150          155          160
Lys Met Glu Arg Val Leu Ile Pro Ala Gly Phe Val Lys Val Thr Ile
    165          170          175
Leu Lys Pro Met Ser Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu

```

SUBSTITUTE SHEET (RULE 26)

1364

```

          180          185          190
Ser Glu Leu Asp Ile Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser
          195          200          205
His Ser Gly Gly Leu Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser
          210          215          220
Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe Ala Ser Ile Met
          225          230          235          240
Gln Glu Met Asp Lys Lys Leu Thr Gln Arg Asn Leu Glu Ser Tyr Gln
          245          250          255
Lys Asp Ala Lys Glu Leu Lys Asn Lys Arg Asn Arg
          260          265

```

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838

```

Ser Asn Phe Lys Lys Gly Phe Phe Met Phe Lys Ser Arg Leu Asn Ser
1          5          10          15
Trp Ile Leu Leu Gly Ile Leu Gly Val Leu Val Val Val Phe Trp Asp
          20          25          30
Val Ile Lys Tyr Lys Ile Glu Asp Leu Gln His Asp His Tyr Leu Ser
          35          40          45
Gln Val Lys Glu Arg Glu Glu Tyr Tyr Lys Asn His Ile Glu Glu Ala
          50          55          60
Leu Lys Lys Asp Ser Glu Cys Phe Glu Lys Gly Gly Asp Lys Val Asp
65          70          75          80
Cys Ser Ala Ala Met Arg Ile Ala Ala Gly Glu Arg Asn Arg Arg Met
          85          90          95
Leu Glu Ile Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839

```

Lys Leu Phe Leu Val Ile Ile Phe Gln Lys Thr Leu Arg Glu Ile Met
1      5      10      15
Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu Ile Leu Ser Lys
20      25      30
Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr Lys Glu Asn Leu
35      40      45
Lys Leu Ile Ala Phe Ile Thr Pro Lys Ile Ser Asn Leu Glu Ile Tyr
50      55      60
Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Met Lys Gly Ser Glu
65      70      75      80
Trp Val Phe Asn Glu Ser Val Leu Thr Pro Leu Ile Lys Glu Leu Lys
85      90      95
Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu Ser Lys Met Ser
100      105      110
Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val
115      120      125
Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn
130      135      140
Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser Ser Ala
145      150      155      160
Ser Lys Val His Ile Ala Leu Asn Leu Leu Trp Thr Ile Arg Asn Arg
165      170      175
Ala Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro Asn Lys Arg Pro
180      185      190
Arg Ile Thr Thr Tyr Phe Ile Gly Leu Lys Asp Asn Asp Arg Ala Arg
195      200      205
Ile Pro Met Asn Ile Ser Val Glu Pro Ser Lys Ile Val Leu Phe Leu
210      215      220
Asp Asp Leu Ile Lys Ser Ile Gly Asn Lys Asp Leu Glu Asp Leu Ser
225      230      235      240
Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840

```

Gly Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu
1      5      10      15
Leu Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp
20      25      30
Asn Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu
35      40      45
Ser Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu

```

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```

50          55          60
Ala Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn
65          70          75          80
Lys Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser
85          90          95
Ile Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser
100         105         110
Phe Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala
115         120         125
Gln Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu
130         135         140
Lys Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr
145         150         155         160
Glu Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala
165         170         175
Asn Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln
180         185         190
Ile Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu
195         200         205
Leu Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys
210         215         220
Ile Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp
225         230         235         240
Tyr Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg
245         250         255
Gln Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala
260         265         270
Ser Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys
275         280         285
Thr Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys
290         295         300
Glu Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val
305         310         315         320
Asn Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg
325         330         335
Asp Ile Ala Gly Lys Lys Gly Glu Ala Ala Ala Lys Val Phe Asn Asp
340         345         350
Tyr Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile
355         360         365
Ala Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln
370         375         380
Met Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile
385         390         395         400
Ile Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu
405         410         415
Glu Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp
420         425         430
Ala Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn
435         440         445
Ser Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe
450         455         460
Asn Pro Tyr
465

```

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841

```

Arg Leu Asn Asn Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser
1      5      10      15
Asn Pro Leu Val Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr
20      25      30
Leu Tyr Pro Asn Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu
35      40      45
Tyr Ser Glu Ile Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu
50      55      60
Lys Gly Ile Gly Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met
65      70      75      80
Val Leu Gly Met Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln
85      90      95
Asn Asn Asp Leu Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe
100     105     110
Val Gly Tyr Leu Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser
115     120     125
Ser Ser Gly Asn Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr
130     135     140
Glu Ile Phe Asp Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn
145     150     155     160
Val Val Lys Glu Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile
165     170     175
Asp Thr His His Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg
180     185     190
Gln Ile Leu Thr Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn
195     200     205
Asn Gly Leu Ser Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val
210     215     220
Ile Leu Gly Leu Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val
225     230     235     240
Phe Met Thr Tyr Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe
245     250     255
Met Leu Leu Leu Gly Phe Phe Gln Gln Thr Arg Gly Phe Leu Val Ser
260     265     270
Tyr Val Lys Lys Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu
275     280     285
Leu Leu Val Leu Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val
290     295     300
Gly Gly Ser Asn Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile
305     310     315     320
Gly Ile Ser Leu Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala
325     330     335
Ile Phe Gly Thr Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr
340     345     350
Gln Gly Val Gln Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser
355     360     365
Leu Lys Ser Val Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr
370     375     380
Lys Asp Ala Lys Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp
385     390     395     400
Met Pro Gly His Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu
405     410     415
Pro Lys Ser His Arg Ala Ser Lys
420

```

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(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842

```

Lys Asn Arg Tyr Leu Lys Arg Gly Arg Asn Ala Ile Leu Glu Pro Ser
1      5      10      15
Arg Asn Arg Leu Lys His Ala Ala Phe Phe Val Gly Leu Phe Ile Val
20      25      30
Leu Phe Leu Ile Ile Met Lys His Gln Thr Ser Pro Tyr Ala Phe Thr
35      40      45
His Asn Gln Ala Leu Val Thr Gln Thr Pro Pro Tyr Phe Thr Gln Leu
50      55      60
Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser Ala His Ala Ser Ser Leu
65      70      75      80
Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser Ala Tyr Phe Ser Gly Thr
85      90      95
Lys Glu Gly Ala Arg Asp Val Lys Ile Ser Ala Asn Leu Phe Asp Ser
100      105      110
Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile Leu Leu Thr Lys Glu Glu
115      120      125
Leu Ser His His Ser His Glu Tyr Ile Lys Lys Leu Gly Asn Pro Leu
130      135      140
Leu Phe Leu His Asp Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser
145      150      155      160
Met Gly Gly Trp Ala Thr Ser Lys Ile Tyr Gln Phe Glu Ser Ala Leu
165      170      175
Glu Pro Ile His Phe Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe
180      185      190
Leu Asn Leu Ser His Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp
195      200      205
Gly Gly Phe Met Leu Pro Leu Tyr His Glu Leu Ala Thr Gln Tyr Pro
210      215      220
Leu Leu Leu Lys Phe Asp Gln Gln Asn Asn Pro Arg Glu Leu Leu Arg
225      230      235      240
Pro Asn Thr Leu Asn His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys
245      250      255
Asp Cys Ala Val Met Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu
260      265      270
Met Leu Glu Thr Cys Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser
275      280      285
Thr Asn Leu Lys Asn Leu Asp Asp Ser Leu Asn Leu Leu Asn Leu Asn
290      295      300
Gly Ile Leu Tyr Leu Ile His Asn Pro Ser Asp Leu Ser Leu Arg Arg
305      310      315      320
Lys Glu Leu Trp Leu Ser Lys Leu Glu Asn Ser Asn Ser Phe Lys Thr
325      330      335
Leu Lys Val Leu Asp Lys Ala Asn Glu Val Ser Tyr Pro Ser Tyr Ser
340      345      350

```

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Leu Asn Pro His Phe Ile Asp Ile Val Tyr Thr Tyr Asn Arg Ser His
 355 360 365
 Ile Lys His Ile Arg Phe Asn Met Ala Tyr Leu Asn Ser Leu Leu Lys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843

Leu Val Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu
 1 5 10 15
 Phe Leu Ile Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe
 20 25 30
 Ser Leu Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp
 35 40 45
 Ser Leu Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser
 50 55 60
 Pro Phe Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His
 65 70 75 80
 Ile Leu Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met
 85 90 95
 Leu Phe Phe Asn Leu Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro
 100 105 110
 Phe Ser Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu
 115 120 125
 Phe Cys Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala
 130 135 140
 Leu Val Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile
 145 150 155 160
 Leu Asp Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys
 165 170 175
 Thr Leu Tyr Leu Ala Lys Lys Arg Leu
 180 185

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844

```

Lys Arg Ile Leu Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe
1      5      10      15
Asn Val Ile Ile Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile
      20      25      30
His Lys Thr Leu Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly
      35      40      45
Lys Leu Gly Ile Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser
      50      55      60
Leu Glu Val Glu Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro
65      70      75      80
Thr Lys Lys Arg Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr
      85      90      95
Gly Ile Trp Ala Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile
      100     105     110
Ile Leu Asp Asp Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys
      115     120     125
Tyr Glu Leu Glu Phe Pro Gly Ile Lys Gly Glu Phe Ser Leu Glu Asp
      130     135     140
Asp Lys Asn Ile Lys Leu Lys Ile Ile Asn Leu Leu Phe Lys Asp Val
145     150     155     160
Lys Val Gln Val Asp Gly Asn Ala His Tyr Ser Pro Lys Ala Arg Lys
      165     170     175
Met Ala Phe Asn Leu Ile Val Lys Pro Leu Val Glu Pro Ser Ala Ala
      180     185     190
Ile Tyr Leu Gln Gly Leu Thr Asp Leu Lys Thr Ile Glu Leu Lys Ile
      195     200     205
Asn Thr Ser Pro Met Lys Ser Leu Ala Phe Leu Lys Pro Leu Phe Gln
      210     215     220
Arg Gln Ser Gln Lys Asn Leu Lys Thr Trp Ile Phe Asp Lys Ile Gln
225     230     235     240
Phe Ala Ser Phe Lys Ile Asp Asn Ala Leu Ile Lys Ala Asn Phe Thr
      245     250     255
Pro Ser Glu Phe Ile Pro Ser Leu Leu Glu Asn Ser Val Val Lys Ala
      260     265     270
Thr Leu Ile Lys Pro Ser Val Val Phe Asn Asp Gly Leu Ser Pro Ile
      275     280     285
Lys Met Asp Lys Thr Glu Leu Ile Phe Lys Asn Lys Gln Leu Leu Ile
      290     295     300
Gln Pro Gln Lys Ile Thr Tyr Glu Thr Met Glu Leu Thr Gly Ser Tyr
305     310     315     320
Ala Thr Phe Ser Asn Leu Leu Glu Ala Pro Lys Leu Glu Val Phe Leu
      325     330     335
Lys Thr Thr Pro Asn Tyr Tyr Gly Asp Ser Ile Lys Asp Leu Leu Ser
      340     345     350
Ala Tyr Lys Val Val Leu Pro Leu Asp Lys Ile Ser Met Pro Ser Ser
      355     360     365
Ala Asp Leu Lys Leu Thr Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu
      370     375     380
Phe Ser Val Gln Gly Ser Val Asn Leu Gln Glu Gly Thr Phe Ser Leu
385     390     395     400
Tyr Asn Ile Pro Leu Tyr Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile
      405     410     415
Ala Gln Glu Tyr Gln Tyr Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr
      420     425     430
Ala Asn Met Leu Asp Leu Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln
      435     440     445
Lys Asn Leu Ser Leu Asp Ser Leu Val His Lys Ile Gln Val Asn Thr
450     455     460

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Asn Asn Asn Ile Asn Met Arg Ser Tyr Asp Pro Asn Asn Thr Gln Glu
 465 470 475 480
 Asp Pro Gln Thr Asn Phe Thr Leu Asp Leu Lys Ser Leu His Ser Ile
 485 490 495
 Ile Gln Glu Gly Glu Asn Ser Glu Val Phe Arg Arg Lys Ile Ile Asp
 500 505 510
 Thr Ile Lys Ala Gln Ser Glu Asp Lys Phe Thr Lys Asp Val Phe Tyr
 515 520 525
 Ala Thr Gly Asp Thr Leu Lys Ser Leu Ser Leu Ser Phe Asp Phe Ser
 530 535 540
 Asn Pro Asp His Ile Gln Trp Ser Val Pro Gln Leu Leu Leu Glu Gly
 545 550 555 560
 Glu Phe Lys Asp Asn Ala Tyr Thr Phe Lys Ile Lys Asp Leu Lys Lys
 565 570 575
 Ile Lys Pro Tyr Ser Pro Ile Met Asp Tyr Ile Ala Leu Lys Asp Gly
 580 585 590
 Ser Leu Glu Val Ser Thr Ser Asp Phe Val Asn Ile Asp Phe Phe Ala
 595 600 605
 Lys Asp Leu Lys Ile Asn Leu Pro Ile Tyr Arg Ser Asp Gly Ser His
 610 615 620
 Phe Asp Ser Phe Ser Leu Phe Gly Ser Ile Asn Lys Asp Glu Ile Ser
 625 630 635 640
 Val Tyr Thr Pro Ser Lys Ser Ile Ser Ile Lys Val Lys Gly Asp Gln
 645 650 655
 Lys Asp Ile Thr Leu Asn Asn Ile Asp Leu Ser Ile Asp Asp Phe Leu
 660 665 670
 Asp Ser Lys Met Pro Ala Ile Ala Gly Leu Phe Ser Lys Glu Arg Lys
 675 680 685
 Glu Lys Pro Ser Ser Lys Glu Ile Gln Asp Glu Asp Val Phe Ile Ser
 690 695 700
 Ala Lys Gln Arg Tyr Glu Lys Ala His Lys Ile Ile Pro Ile Ser Thr
 705 710 715 720
 Arg Ile His Ala Lys Asp Val Val Leu Ile Tyr Lys Lys Met Pro Phe
 725 730 735 740
 Pro Leu Glu Asn Leu Asp Ile Val Ala Gln Asp Asp Arg Val Lys Ile
 745 750
 Asp Gly Asn Tyr Lys Asn Ala Met Ile Met Ala Asp Leu Val His Gly
 755 760 765
 Ala Leu Tyr Leu Lys Ala His Asn Phe Ser Gly Asp Tyr Ile Asn Thr
 770 775 780
 Ile Leu Gln Lys Asp Phe Val Glu Gly Gly Leu Phe Thr Leu Ile Gly
 785 790 795 800
 Ala Leu Glu Asp Gln Val Phe Asn Gly Glu Leu Lys Phe Gln Asn Thr
 805 810 815
 Ser Leu Lys Asn Phe Ala Leu Met Gln Asn Met Val Asn Leu Ile Asn
 820 825 830
 Thr Ile Pro Ser Leu Ile Val Phe Arg Asn Pro His Leu Gly Ala Asn
 835 840 845
 Gly Tyr Gln Ile Lys Thr Gly Ser Val Val Phe Gly Ile Thr Lys Glu
 850 855 860
 Tyr Leu Gly Leu Glu Lys Ile Asp Leu Val Gly Lys Thr Leu Asp Ile
 865 870 875 880
 Ala Gly Asn Gly Ile Ile Glu Leu Asp Lys Asn Lys Leu Asp Leu Asn
 885 890 895
 Leu Glu Val Ser Thr Ile Lys Ala Leu Ser Asn Val Leu Asn Lys Ile
 900 905 910
 Pro Ile Val Gly Tyr Leu Val Leu Gly Lys Gly Gly Lys Ile Thr Thr
 915 920 925
 Asn Val Asn Val Lys Gly Thr Leu Asp Lys Pro Lys Thr Gln Val Thr
 930 935 940
 Leu Ala Ser Asp Ile Ile Gln Ala Pro Phe Lys Ile Leu Arg Arg Ile
 945 950 955 960
 Phe Thr Pro Ile Asp Ile Ile Val Asp Glu Val Lys Lys Asn Ile Asp
 965 970 975
 Ser Lys Arg Lys Leu Lys

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(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845

```

Arg Pro Phe Arg Ser Leu Ile Arg Ile Thr His Ala Pro Lys Leu Lys
1      5      10      15
Pro Ser Phe Ala Leu Glu Cys Val Ile Thr Trp Glu Ala Ile Asn Ser
20      25      30
Met Glu Ile Thr Leu Phe Asp Pro Ile Asp Ala His Leu His Val Arg
35      40      45
Glu Asn Ala Leu Leu Lys Ala Val Leu Glu Tyr Ser Ser Glu Pro Phe
50      55      60
Ser Ala Ala Val Ile Met Pro Asn Leu Ser Lys Pro Leu Ile Asp Thr
65      70      75      80
Pro Ile Thr Leu Glu Tyr Glu Glu Glu Ile Leu Lys Asn Ser Ser Asn
85      90      95
Phe Lys Pro Leu Met Ser Leu Tyr Phe Asn Asp Gly Leu Thr Leu Glu
100     105     110
Glu Leu Gln Arg Ala Lys Asn Lys Gly Ile Lys Phe Leu Lys Leu Tyr
115     120     125
Pro Lys Gly Met Thr Thr Asn Ala Gln Asn Gly Thr Ser Asp Leu Leu
130     135     140
Gly Glu Lys Thr Leu Glu Val Leu Glu Asn Ala Gln Lys Leu Gly Phe
145     150     155     160
Ile Leu Cys Val His Ala Glu Gln Ala Gly Phe Cys Leu Asp Lys Glu
165     170     175
Phe Leu Cys His Ser Val Leu Glu Thr Phe Ala Leu Ser Phe Pro Lys
180     185     190
Leu Lys Ile Ile Ile Glu His Leu Ser Asp Trp Arg Ser Ile Ala Leu
195     200     205
Ile Glu Lys His Asp Asn Leu Tyr Ala Thr Leu Thr Leu His His Ile
210     215     220
Ser Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys
225     230     235     240
Phe Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu
245     250     255
Ser Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Ser Asp Ser
260     265     270
Ala Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly
275     280     285
Ile Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu
290     295     300
Lys His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala
305     310     315     320
Lys Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu
325     330     335

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Ser Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu
 340 345 350
 Lys Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln
 355 360 365
 Glu Ile Ala
 370

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846

Glu Ile Tyr Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly
 1 5 10 15
 Lys Asn Phe Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser
 20 25 30
 Leu Ile Leu Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu
 35 40 45
 His Arg Glu Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn
 50 55 60
 Pro Glu Asn Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser
 65 70 75 80
 Lys Asn Asn Pro Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys
 85 90 95
 Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Lys Pro
 100 105 110
 Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro
 115 120 125
 Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val
 130 135 140
 Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Glu Lys Lys Val Val
 145 150 155 160
 Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys Lys Pro Val Lys
 165 170 175
 Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro Lys Glu Val Ala
 180 185 190
 Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn Gln Thr Arg Arg
 195 200 205
 Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp Leu Gly Thr Ala
 210 215 220
 Arg Lys Arg Phe His Gln Glu
 225 230

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847

```

Ser Arg Tyr His Pro Arg Gly Phe Ser Gln Leu Pro Lys Leu Lys Leu
1          5          10          15
Ile Cys Ile Thr Ala Thr Gly Thr Asp Asn Val Asp Ile Lys Ser Ala
20          25          30
Lys Ala Leu Gly Ile Glu Val Lys Asn Val Ser Ala Tyr Ser Thr Glu
35          40          45
Ser Val Ala Gln His Thr Leu Ala Cys Ala Leu Ser Leu Leu Gly Arg
50          55          60
Ile Asn Asp Tyr Asp Arg Tyr Cys Lys Ser Gly Glu Tyr Ser Gln Ser
65          70          75          80
Asp Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly
85          90          95
Gly Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala
100         105         110
Lys Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys
115         120         125
Asp Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Leu Leu Lys
130         135         140
Thr Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg
145         150         155         160
Asp Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile
165         170         175
Leu Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Asp Leu Ala
180         185         190
Leu Ile Leu Glu Thr Lys Asp Leu Tyr Tyr Ala Ser Asp Val
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848

```

Ile Leu Glu Asn Leu Arg Ile Tyr Ala Arg Leu Leu Glu Met Ile Leu
1          5          10          15

```

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```

Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu Ile Phe Ile
      20      25      30
Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn Glu Val Ala
      35      40      45
Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe Pro Asn Tyr
      50      55      60
Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp Ala Lys Ser
      65      70      75      80
Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn Leu Ser Tyr
      85      90      95
Val Asn Asp Phe Ile Ser Lys Val Gln Lys
      100      105

```

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849

```

Cys Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys
1      5      10      15
Met Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln
      20      25      30
Ile Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly
      35      40      45
Ile Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys
      50      55      60
Ala Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn
      65      70      75      80
Phe Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala
      85      90      95
Phe Gly Asn Asp Thr Lys Lys Phe Asp Phe Val Ile Phe Ser Lys Glu
      100      105      110
Lys Thr Tyr Phe His Arg Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850

```

Leu Val Ile Asn Ser Lys Thr Gly Leu Leu Thr Ile Lys Gly Glu Asp
1          5          10          15
Ala Leu Gly Lys Ala Ser Leu Lys Asp Leu Gly Leu Ser Ala Gly Met
          20          25          30
Val Gln Ser Tyr Glu Ala Ser Gln Asp Thr Leu Phe Met Ser Lys Asn
          35          40          45
Leu Gln Lys Ala Ser Asp Ser Gln Phe Thr Tyr Asn Gly Val Ser Ile
          50          55          60
Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser Gly Val Asn Ile
          65          70          75          80
Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala Ile Ile Ser Val
          85          90          95
Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys Glu Phe Val Lys
          100         105         110
Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp Thr Arg Tyr Asp
          115         120         125
Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val Gly Asp Ile Arg
          130         135         140
Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr Ser Val His Thr
          145         150         155         160
Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu Ser Leu Asp Asp
          165         170         175
Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser Ser Ala Leu Asn
          180         185         190
Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly Ser Asp Ser Lys
          195         200         205
Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile Phe Ser Lys Phe
          210         215         220
Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn Ala Lys Leu Lys
          225         230         235         240
Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser Leu Thr Lys Asp
          245         250         255
Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr Asn Ile Met Ala
          260         265         270
Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys Ala Asn Gln Lys
          275         280         285
Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala Ala Lys Lys Asn
          290         295         300

```

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...129

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851

```

Arg Asn Ile Met Gln Tyr Ala Asn Ala Tyr Gln Ala Tyr Gln His Asn
1      5      10      15
Arg Val Ser Val Glu Ser Pro Ala Lys Leu Ile Glu Met Leu Tyr Glu
      20      25      30
Gly Ile Leu Arg Phe Ser Ser Gln Ala Lys Arg Cys Ile Glu Asn Glu
      35      40      45
Asp Ile Glu Lys Lys Ile Tyr Tyr Ile Asn Arg Val Thr Asp Ile Phe
      50      55      60
Thr Glu Leu Leu Asn Ile Leu Asp Tyr Glu Lys Gly Gly Lys Val Ala
      65      70      75      80
Val Tyr Leu Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln
      85      90      95
Ala Asn Val Glu Asn Asp Ala Ser Lys Ile Asp Leu Val Leu Asn Val
      100      105      110
Ala Arg Gly Leu Leu Glu Ala Trp Arg Glu Ile His Ser Asp Glu Leu
      115      120      125
Ala

```

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852

```

Phe Asp Asp Leu Tyr Gly Ser Asn Ser Leu Pro Phe Tyr Pro Arg Val
1      5      10      15
Thr Pro Val Lys Phe Pro Thr Phe Lys Trp Ala Leu Leu Lys Ala Leu
      20      25      30
Ile Lys Asp Asp Phe Pro Thr Leu Gly Trp Pro Thr Arg Ala Thr Met
      35      40      45
Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu Ile
      50      55      60
Phe Gly Tyr Ile Val Phe Lys Ser Trp His Tyr Ser Ala Ile Arg Leu
      65      70      75      80
Ile Val Ile

```

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853

```

Lys Arg Asp Lys Asn Val Lys Met Arg Lys Gly Arg Val Met Leu Cys
1      5      10      15
Val Phe Asp Ile Glu Thr Ile Pro Asn Ile Ser Leu Cys Lys Glu His
20      25      30
Phe Gln Leu Lys Glu Asp Asp Ala Leu Lys Ile Cys Glu Trp Ser Phe
35      40      45
Glu Lys Gln Lys Glu Lys Ser Gly Ser Glu Phe Leu Pro Leu Tyr Leu
50      55      60
His Glu Ile Ile Ser Ile Ala Ala Val Ile Gly Asp Asp Tyr Gly Gln
65      70      75      80
Phe Ile Lys Val Gly Asn Phe Gly Gln Lys His Glu Asn Lys Glu Asp
85      90      95
Phe Ala Ser Glu Lys Glu Leu Leu Glu Asp Phe Phe Lys Tyr Phe Asn
100     105     110
Glu Lys Gln Pro Arg Leu Ile Ser Phe Asn Gly Arg Gly Phe Asp Ile
115     120     125
Pro Leu Leu Thr Leu Lys Ala Leu Lys Tyr Asn Leu Thr Leu Asp Ala
130     135     140
Phe Tyr Ser Gln Glu Asn Lys Trp Glu Asn Tyr Arg Ala Arg Tyr Ser
145     150     155     160
Glu Gln Phe His Leu Asp Leu Met Asp Ser Leu Ser His Tyr Gly Ser
165     170     175
Val Arg Gly Leu Asn Leu Asn Gly Val Cys Ser Met Thr Asn Ile Pro
180     185     190
Gly Lys Phe Asp Val Ser Gly Asp Leu Val His Ala Ile Tyr Tyr Asn
195     200     205
Pro His Leu Arg Pro Lys Gly Gly Lys Arg His Tyr
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854

```

Arg Phe Lys Ala Arg Ile Val Arg Phe Phe Ile Phe Leu Ile Leu Ile
1      5      10      15
Cys Pro Leu Ile Cys Pro Leu Met Ser Ala Asp Ser Ala Leu Pro Ser
20      25      30

```

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```

Val Asn Leu Ser Leu Asn Ala Pro Ser Asp Pro Lys Gln Leu Val Thr
   35           40           45
Thr Leu Asn Val Ile Ala Leu Leu Thr Leu Leu Val Leu Ala Pro Ser
   50           55           60
Leu Ile Leu Val Met Thr Ser Phe Thr Arg Leu Ile Val Val Phe Ser
   65           70           75           80
Phe Leu Arg Thr Ala Leu Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile
   85           90           95
Leu Val Ser Leu Ser Leu Ile Leu Thr Phe Phe Ile Met Glu Pro Ser
   100          105          110
Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys
   115          120          125
Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu
   130          135          140
Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg
   145          150          155          160
Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Asp Val Ser Leu Ser
   165          170          175
Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys Thr Ala Phe Gln
   180          185          190
Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile Asp Met Val Ile
   195          200          205
Ser Ser Ile Leu Met Ala Met Gly Met Met Met Leu Pro Pro Val Met
   210          215          220
Ile Ser Leu Pro Phe Lys Ile Leu Val Phe Ile Leu Val Asp Gly Phe
   225          230          235          240
Asn Leu Leu Thr Glu Asn Leu Val Ala Ser Phe Lys Met Val
   245          250

```

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855

```

Lys Trp Gly Ile Leu Pro Gly Leu Pro Val Asp Lys Met Glu Val Ser
1           5           10           15
Leu Ile His Lys Asp His Gln Ile Thr Ile Ile Asp Leu Pro Gly Thr
   20           25           30
Tyr Ala Leu Asn Asp Phe Thr Thr Glu Glu Lys Val Thr Lys Asp Phe
   35           40           45
Leu Glu Lys Gly Gln Tyr Asn Leu Ile Leu Asn Val Val Asp Ser Thr
   50           55           60
Asn Leu Glu Arg Asn Leu Ala Leu Ser Ala Gln Leu Leu Asp Thr Asn
   65           70           75           80
Lys Lys Met Leu Leu Ala Leu Asn Met Trp Asp Glu Ala Lys Lys Glu
   85           90           95
Gly Ile Asn Ile Asn Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val
   100          105          110
Cys Val Pro Thr Ser Ala Arg Ser Lys Glu Asp Arg Leu Asn Thr Glu

```

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115 120 125
 Leu Leu Leu Asp Glu Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn
 130 135 140
 Asn Glu Asn Ile Lys Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys
 145 150 155 160
 Tyr Ser Gln Ser Ala Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn
 165 170 175
 Lys Gln Asn Ala Ser Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Leu
 180 185 190
 Met His Gln Arg Tyr Gly Ile Phe Ile Phe Leu Gly Phe Met Phe Ile
 195 200 205
 Ile Phe Ser Leu Ser Phe Leu Ile Gly Gly Gly Val Gln Lys Ala Leu
 210 215 220
 Glu Glu Gly Phe Lys Ile Leu Ser Asp Ser Ile Lys Glu Asn Val Ala
 225 230 235 240
 Asn Glu Asp Leu Ala Ser Leu Val Gly Asp Gly Ile Ile Gly Gly Val
 245 250 255
 Gly Ala Thr Val Ser Phe Leu Pro Leu Ile Val Val Leu Tyr Phe Gly
 260 265 270
 Ile Ser Leu Leu Glu Thr Thr Gly Tyr Met Ser Arg Val Ala Phe Leu
 275 280 285
 Leu Asp Gly Ile Leu His Lys Phe Gly Leu His Gly Lys Ser Phe Ile
 290 295 300
 Pro Leu Ile Thr Gly Phe Gly Cys Ser Val Pro Ala Tyr Met Ala Thr
 305 310 315 320
 Arg Thr Leu Gln Asn Tyr Asn Glu Arg Leu Ile Thr Leu Phe Val Ile
 325 330 335
 Gly Phe Met Ser Cys Ser Ala Arg Leu Pro Ile Tyr Val Leu Phe Val
 340 345 350
 Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe Val Leu Phe Cys Ile
 355 360 365
 Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met Ala Lys Leu Leu Lys
 370 375 380
 Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe Ile Met Glu Met Pro
 385 390 395 400
 Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr Phe Ser Ile Tyr Thr
 405 410 415
 Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr Tyr Ile Leu Val Gly
 420 425 430
 Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro Lys Asn Asp Ala Ala
 435 440 445
 Met Lys Thr Tyr Lys Gln Glu Ser Leu Leu Val Gln Lys Asn Ala Asn
 450 455 460
 Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys Glu Leu Lys Thr Glu
 465 470 475 480
 Leu Asp Lys Lys Asn Leu Lys Asn Ser Val Val Gly Arg Gly Gly Ala
 485 490 495
 Tyr Leu Glu Lys Val Phe Asn Pro Met Asp Phe Asp Trp Arg Leu Ser
 500 505 510
 Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu Val Val Val Ser Thr
 515 520 525
 Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn Glu Lys Ser Asp Ala
 530 535 540
 Phe Arg Glu Ile Ile Arg Lys Glu Val Ser Val Pro Ser Gly Ile Ala
 545 550 555 560
 Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys Phe Ala Ala Thr Ile
 565 570 575
 Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe Val Ala Tyr Leu Phe
 580 585 590
 Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser Leu Ile Ala Phe Tyr
 595 600 605
 Ala Thr Gln Ile Leu Val
 610

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(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856

```

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1      5      10      15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
20      25      30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
35      40      45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
50      55      60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65      70      75      80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
85      90      95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
100      105      110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
115      120      125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
130      135      140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145      150      155      160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
165      170      175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
180      185      190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
195      200      205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
210      215      220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225      230      235      240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
245      250      255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
260      265      270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
275      280      285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
290      295      300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305      310      315      320
Gly Gly Phe His Phe
325

```

(2) INFORMATION FOR SEQ ID NO:1857:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857

```

Arg Leu Lys Pro Asn Val Ile Glu Arg Arg Met Leu Glu Lys Leu Leu
1          5          10          15
Ser Ala Ile Lys Gln Lys Val Ser Asn Tyr Phe Leu Gly Val Leu Pro
20          25          30
Lys Ser Tyr Ser Met Ser Glu Glu Asn Asn Ile Leu Gly Leu Tyr Asp
35          40          45
Glu His Phe Leu Leu Thr Lys Asn Glu Asn Leu Val Gly Ile Leu Arg
50          55          60
Leu Glu Gly Val Ser Tyr Thr His Leu Ser Thr Glu Gln Leu Gln Asp
65          70          75          80
Leu Phe Thr Glu Arg Gln Met Ala Leu Asp Ser Leu Glu Lys Val Val
85          90          95
Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser Ile
100         105         110
Gln Ser Asp Ser Gln Tyr Leu Gln Ala Ile Leu Asn Gln Phe Glu Asn
115         120         125
Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr His
130         135         140
Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His Ala
145         150         155         160
Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe Leu
165         170         175
Gln Glu Thr Leu Lys Ser Leu Glu Ile Gln Leu Lys Asn Tyr Ala Pro
180         185         190
Lys Leu Leu Asn Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile
195         200         205
Asn Gly Phe Glu Leu Pro Leu Lys Pro Leu Val Gly Gly Tyr Leu Ser
210         215         220
Asp Ser Tyr Ile Ala Ser Ser Ile Thr Phe Glu Lys Asp Tyr Phe Ile
225         230         235         240
Gln Glu Ser Phe Asn Gln Lys Thr Tyr Asn Arg Leu Ile Gly Ile Lys
245         250         255
Ala Tyr Glu Ser Glu Arg Ile Thr Ser Ile Ala Val Gly Ala Leu Leu
260         265         270
Tyr Gln Glu Thr Pro Leu Asp Ile Ile Phe Ser Ile Glu Pro Met Ser
275         280         285
Val Asn Lys Thr Leu Ser Phe Leu Lys Glu Arg Ala Lys Phe Ser Met
290         295         300
Ser Asn Leu Val Lys Asn Glu Leu Leu Glu Tyr Gln Glu Leu Val Lys
305         310         315         320
Thr Lys Arg Leu Ser Met Gln Lys Phe Ala Leu Asn Val Leu Ile Lys
325         330         335
Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu Gly
340         345         350
Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly Leu
355         360         365

```

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Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn His
 370 375 380
 Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val Phe
 385 390 395 400
 Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser Pro
 405 410 415
 Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn Phe
 420 425 430
 His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg Val
 435 440 445
 Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser Thr
 450 455 460
 Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met Arg
 465 470 475 480
 Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu Phe
 485 490 495
 Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro Phe
 500 505 510
 Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe Phe
 515 520 525
 Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu Glu
 530 535 540
 Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr Leu
 545 550 555 560
 Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys Arg
 565 570 575
 Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn Asn
 580 585 590
 Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe Leu
 595 600 605
 Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu Gly
 610 615 620
 Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg Lys
 625 630 635 640
 Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr Val
 645 650 655
 Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln Ala
 660 665 670
 Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr Gln
 675 680 685
 Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly Thr
 690 695 700
 Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn Phe
 705 710 715 720
 Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr Pro
 725 730 735
 Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser Ser
 740 745 750
 Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys Ile
 755 760 765
 Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln Lys
 770 775 780
 Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
 785 790 795

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858

```

Lys Met Ile Leu Lys Ser Ser Ile Asp Arg Leu Leu Gln Thr Ile Asp
1      5      10      15
Ile Val Glu Val Ile Ser Ser Tyr Val Asp Leu Arg Lys Ser Gly Ser
20      25      30
Asn Tyr Met Ala Cys Cys Pro Phe His Glu Glu Arg Ser Ala Ser Phe
35      40      45
Ser Val Asn Gln Val Lys Gly Phe Tyr Tyr Cys Phe Gly Cys Gly Ala
50      55      60
Ser Gly Asp Ser Ile Lys Phe Val Met Ala Phe Glu Lys Leu Ser Phe
65      70      75      80
Val Glu Ala Leu Glu Lys Leu Ala His Arg Phe Asn Ile Ala Leu Glu
85      90      95
Tyr Asp Lys Gly Val Tyr Tyr Asp His Lys Glu Asp Tyr His Leu Leu
100      105      110
Glu Met Val Ser Ser Leu Tyr Gln Glu Glu Leu Phe Asn Ala Pro Phe
115      120      125
Phe Leu Asn Tyr Leu Gln Lys Arg Gly Leu Ser Met Glu Ser Ile Lys
130      135      140
Ala Phe Lys Leu Gly Leu Cys Thr Asn Lys Ile Asp Tyr Gly Ile Glu
145      150      155      160
Asn Lys Gly Leu Asn Lys Asp Lys Leu Ile Glu Leu Gly Val Leu Gly
165      170      175
Lys Ser Asp Lys Glu Asp Lys Thr Tyr Leu Arg Phe Leu Asp Arg Ile
180      185      190
Met Phe Pro Ile Tyr Ser Pro Ser Ala Gln Val Val Gly Phe Gly Gly
195      200      205
Arg Thr Leu Lys Glu Lys Ala Ala Lys Tyr Ile Asn Ser Pro Gln Asn
210      215      220
Lys Leu Phe Asp Lys Ser Ser Leu Leu Tyr Gly Tyr His Leu Ala Lys
225      230      235      240
Glu His Ile Tyr Lys Gln Lys Gln Val Ile Val Thr Glu Gly Tyr Leu
245      250      255
Asp Val Ile Leu Leu His Gln Ala Gly Phe Lys Asn Ala Ile Ala Thr
260      265      270
Leu Gly Thr Ala Leu Thr Pro Ser His Leu Pro Leu Leu Lys Lys Gly
275      280      285
Asp Pro Glu Ile Leu Leu Ser Tyr Asp Gly Asp Lys Ala Gly Arg Asn
290      295      300
Ala Ala Tyr Lys Ala Ser Leu Met Leu Ala Lys Glu Gln Arg Lys Gly
305      310      315      320
Gly Val Ile Leu Phe Glu Asn Asn Leu Asp Pro Ala Asp Met Ile Ala
325      330      335
Asn His Gln Ile Glu Thr Leu Lys Asn Trp Leu Ser Arg Pro Ile Ala
340      345      350
Phe Ile Glu Phe Val Leu Arg His Met Ala Gly Ser Tyr Leu Leu Asp
355      360      365
Asp Pro Leu Glu Lys Asp Lys Ala Leu Lys Glu Met Leu Gly Phe Leu
370      375      380
Lys Asn Phe Ser Leu Leu Leu Gln Asn Glu Tyr Lys Pro Leu Ile Ala
385      390      395      400
Thr Leu Leu Gln Ala Pro Leu His Val Leu Gly Ile Arg Glu Pro Val
405      410      415
Ser Phe Gln Pro Phe Tyr Pro Lys Thr Glu Lys Pro Asn Arg Pro Gln
420      425      430

```

SUBSTITUTE SHEET (RULE 26)

```

Lys Phe Ala His Val Ser Ser Met Pro Ser Leu Glu Phe Leu Glu
    435                      440                      445
Leu Val Ile Arg Tyr Leu Leu Glu Asp Arg Ser Leu Leu Asp Leu Ala
    450                      455                      460
Val Gly Tyr Ile His Ser Gly Val Phe Leu His Lys Lys Gln Glu Phe
    465                      470                      475                      480
Asp Ala Leu Cys Gln Glu Lys Leu Asp Asp Pro Lys Leu Val Ala Leu
    485                      490                      495
Leu Leu Asp Ala Asn Leu Pro Leu Lys Lys Gly Gly Phe Glu Lys Glu
    500                      505                      510
Leu Arg Leu Leu Ile Leu Arg Tyr Phe Glu Pro Pro Thr Gln Arg Asn
    515                      520                      525
Pro

```

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859

```

Leu Arg Gly His Arg Arg Thr Tyr Ile Gly Ser Met Pro Gly Arg Ile
1      5      10      15
Val Gln Gly Leu Ile Glu Ala Lys Lys Met Asn Pro Val Met Val Leu
    20      25      30
Asp Glu Ile Asp Lys Val Asp Arg Ser Val Arg Gly Asp Pro Ala Ser
    35      40      45
Ala Leu Leu Glu Ile Leu Asp Pro Glu Gln Asn Ile Ala Phe Arg Asp
    50      55      60
His Tyr Ala Asn Phe Ser Ile Asp Leu Ser Gln Val Ile Phe Ile Ala
    65      70      75      80
Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro Leu Arg Asp Arg Met
    85      90      95
Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser Glu Lys Glu Glu Ile
    100     105     110
Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu Lys His Ala Leu Lys
    115     120     125
Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu Lys Leu Ile Ile Glu
    130     135     140
Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu Arg Arg Gln Ile Ala
    145     150     155     160
Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu Glu Asp Asn Pro His
    165     170     175
Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys Asp Lys Lys Gly Gly
    180     185     190
Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys Asp Phe Cys Val Ser
    195     200     205
Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu Arg Met Val Phe Glu
    210     215     220
Ile Asp Pro Ile Asp Glu Glu Asn Lys Ile Gly Ile Val Asn Gly Leu

```

SUBSTITUTE SHEET (RULE 26)

```

225          230          235          240
Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys Ile Glu Ala Val Lys
          245          250          255
Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly Ser Leu Gly Asp Val
          260          265          270
Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val Val Lys Val Leu Leu
          275          280          285
Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro Ser Glu Thr Asp Ala
          290          295          300
Glu Asn Lys Lys Lys Lys Lys Val Leu Lys Val Tyr Asn Ala Tyr Asp
305          310          315          320
Leu His Leu His Val Pro Glu Gly Ala Thr Pro Lys Asp Gly Pro Ser
          325          330          335
Ala Gly Ile Ala Met Ala Ser Val Met Ala Ser Ile Leu Cys Asp Arg
          340          345          350
Ala Ile Arg Ser Glu Val Ala Met Thr Gly Glu Leu Thr Leu Ser Gly
          355          360          365
Glu Val Leu Pro Ile Gly Gly Leu Lys Glu Lys Leu Ile Ala Ala Phe
          370          375          380
Lys Ala Gly Ile Lys Thr Ala Leu Ile Pro Val Lys Asn Tyr Glu Arg
385          390          395          400
Asp Leu Asp Glu Ile Pro Thr Glu Val Arg Glu Asn Leu Asn Ile Val
          405          410          415
Ala Val Lys Asn Ile Ala Glu Val Leu Glu Lys Thr Leu Leu
          420          425          430

```

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860

```

Lys Arg Tyr Arg Lys Thr Ala Leu Leu Arg Leu Asp Asn Gly Asp Lys
1          5          10          15
Leu Ser Leu Met Arg Glu Phe Phe Lys Ser Val Arg Gly Phe Leu Asn
          20          25          30
Leu Leu Arg Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly
          35          40          45
Leu Ser Glu Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile
          50          55          60
Leu Ser Leu Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser
          65          70          75          80
His Tyr Leu Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro
          85          90          95
Asn Ala Pro Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe
          100          105          110
Lys Lys Thr Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val
          115          120          125
Val Ala Leu Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys
          130          135          140

```

SUBSTITUTE SHEET (RULE 26)

1387

```

Ile Phe Asp Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu
145          150          155          160
Ile Phe Leu Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala
          165          170          175
Leu Pro Leu Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu
          180          185          190
Asp Lys Asp Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr
          195          200          205
Ala Phe Phe Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys
          210          215          220
His Tyr Phe Trp Val Phe Leu Trp Val Phe Phe Thr Ser Val Ser Trp
225          230          235          240
His Val Leu Lys Trp Ala Ser Thr Leu Phe Met Cys Tyr Thr Asn Pro
          245          250          255
His Leu Leu Met Ser Leu Tyr Gly Ser Arg Phe Pro Phe Cys Gly Phe
          260          265          270

```

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861

```

Val Gly Val Val Met Ile Lys Lys Thr Leu Ala Ser Val Leu Leu Gly
1          5          10          15
Leu Ser Leu Met Ser Val Leu Asn Ala Lys Glu Cys Val Ser Pro Ile
          20          25          30
Thr Arg Ser Val Lys Tyr His Gln Ser Ala Glu Ile Arg Ala Leu
          35          40          45
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
          50          55          60
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
65          70          75          80
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
          85          90          95
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
          100          105          110
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
          115          120          125
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
          130          135          140
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
145          150          155          160
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
          165          170          175
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
          180          185          190
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
          195          200          205
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr

```

SUBSTITUTE SHEET (RULE 26)

1388

210 215 220
 Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
 225 230 235 240
 Pro Ile Lys Ala Trp Gln Asn Lys Lys
 245

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862

His Asp Lys Lys Phe Asp Leu Leu Gly Gly Val Met Asp Phe Val Gly
 1 5 10 15
 Phe Glu Asp Leu Lys Cys Lys Asp Lys Glu Asn Ser Gln Lys Val Phe
 20 25 30
 Val Ile Arg Asn Asp Lys Leu Gly Asp Phe Ile Leu Val Ile Pro Ala
 35 40 45
 Leu Ile Ala Leu Lys His Ala Phe Leu Glu Lys Gly Val Glu Val Tyr
 50 55 60
 Leu Gly Val Val Val Pro Ser Tyr Thr Thr Pro Ile Ala Leu Glu Phe
 65 70 75 80
 Pro Phe Ile Asp Glu Val Ile Ile Glu Asp Asn His Leu Ala Thr Thr
 85 90 95
 Pro Lys Asn Arg Ser Thr Asp Ala Leu Ile Phe Leu Phe Ser Asn Phe
 100 105 110
 Lys Asn Ala Lys Leu Ala Phe Ser Leu Arg Lys Ser Ile Pro Tyr Ile
 115 120 125
 Leu Ala Pro Lys Thr Lys Ile Tyr Ser Trp Leu Tyr Gln Lys Arg Val
 130 135 140
 Arg Gln Asn Arg Ser Leu Cys Leu Lys Thr Glu Tyr Glu Tyr Asn Leu
 145 150 155 160
 Asp Leu Ile His Ala Phe Cys Lys Asp Tyr Asp Leu Pro Asn Ala Gln
 165 170 175
 Leu Lys Lys Ile Ala Trp Lys Leu Lys Asp Lys Ser Lys Glu Arg Ser
 180 185 190
 Ile Ile Ala Ser Lys Leu Asn Ala Asn Val Asp Leu Leu Trp Ile Gly
 195 200 205
 Val His Met His Ser Gly Gly Ser Ser Pro Val Leu Pro Ala Ser His
 210 215 220
 Phe Ile Glu Leu Ile Ala Ile Leu His Glu Lys Leu Ser Cys Glu Ile
 225 230 235 240
 Ile Leu Ile Cys Gly Pro Gly Glu Arg Lys Ala Thr Glu Glu Leu Leu
 245 250 255
 Lys Glu Val Pro Phe Ala His Leu Tyr Asp Thr Ser His Ser Leu Val
 260 265 270
 Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val Cys Ile Gly Asn Ala
 275 280 285
 Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp Asn Gln Ser Ile Gly
 290 295 300

SUBSTITUTE SHEET (RULE 26)

1389

```

Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala Arg Trp Arg Pro Phe
305                      310                      315                      320
Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn Gly Ser Asn Asp Met
                      325                      330                      335
Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys Ile Met Gly Phe Ile
                      340                      345                      350
Thr Lys Asn Leu Ser His His Met Gln Glu Arg
                      355                      360

```

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863

```

Gly Asn Thr Ile Ile Lys Met Gln Lys Ser Leu Ile Thr Thr Pro Ile
1      5      10      15
Tyr Tyr Val Asn Asp Ile Pro His Ile Gly His Ala Tyr Thr Thr Leu
20      25      30
Ile Ala Asp Thr Leu Lys Lys Tyr Tyr Thr Leu Gln Gly Glu Glu Val
35      40      45
Phe Phe Leu Thr Gly Thr Asp Glu His Gly Gln Lys Ile Glu Gln Ser
50      55      60
Ala Arg Leu Arg Asn Gln Ser Pro Lys Ala Tyr Ala Asp Ser Ile Ser
65      70      75      80
Ala Ile Phe Lys Asn Gln Trp Asp Phe Phe Asn Leu Asp Tyr Asp Gly
85      90      95
Phe Ile Arg Thr Thr Asp Ser Glu His Gln Lys Cys Val Gln Asn Ala
100     105     110
Phe Glu Ile Met Phe Glu Lys Gly Asp Ile Tyr Lys Gly Thr Tyr Ser
115     120     125
Gly Tyr Tyr Cys Val Ser Cys Glu Ser Tyr Cys Ala Val Ser Lys Val
130     135     140
Asp Asn Thr Asp Ser Lys Val Leu Cys Pro Asp Cys Leu Arg Glu Thr
145     150     155     160
Thr Leu Leu Glu Glu Glu Ser Tyr Phe Phe Lys Leu Ser Ala Tyr Glu
165     170     175
Lys Pro Leu Leu Glu Phe Tyr Ala Lys Asn Pro Glu Ala Ile Leu Pro
180     185     190
Ile Tyr Arg Lys Asn Glu Val Thr Ser Phe Ile Glu Gln Gly Leu Leu
195     200     205
Asp Leu Ser Ile Thr Arg Thr Ser Phe Glu Trp Gly Ile Pro Leu Pro
210     215     220
Lys Lys Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala
225     230     235     240
Leu Leu Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn
245     250     255
Lys Met Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile
260     265     270
Leu Arg Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn

```

SUBSTITUTE SHEET (RULE 26)

1390

```

      275              280              285
Leu Pro Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu
 290      295      300
Gly Val Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys
305      310      315      320
Leu Ala Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg
      325      330      335
Glu Val Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val
      340      345      350
Glu Arg Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn
      355      360      365
Arg Leu Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser
      370      375      380
Thr Lys Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln
385      390      395      400
Ile Leu Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys
      405      410      415
Ala Leu Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile
      420      425      430
Ala Lys Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys
      435      440      445
Leu Glu Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser
      450      455      460
Phe Leu Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser
      465      470      475      480
Ala Phe Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys
      485      490      495
Ala Lys Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe
      500      505      510
Ser Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu
      515      520      525
Lys Ile Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys
      530      535      540
Glu Lys Glu Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu
      545      550      555      560
Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln
      565      570      575
Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly
      580      585      590
Glu Asn Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu
      595      600      605
Pro Glu Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys
      610      615      620
Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val
      625      630      635      640
Arg Asp Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile
      645      650      655
Ala Gly Ser Leu Ile Ser
      660

```

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

1391

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864

```

Gly Arg Met Met Lys Ile Val Ile Asp Leu Met Gly Ala Asp His Gly
1      5      10      15
Val Leu Pro Ile Ile Glu Gly Val Ser Arg Ala Leu Glu Asn Lys Ser
20      25      30
Phe Ser Val Val Leu Val Gly Asp Lys Asp Lys Ala Thr Pro Phe Ile
35      40      45
Ser Lys Glu Leu Ala Ser Lys Val Glu Met Ile His Thr Gln Asp Tyr
50      55      60
Ile Lys Met Glu Glu Ala Ala Thr Glu Ala Ile Lys Arg Lys Glu Ser
65      70      75      80
Ser Ile Tyr Leu Gly Met Asp Ile Leu Lys Asn Gly Ala Asp Ala Leu
85      90      95
Ile Ser Ala Gly His Ser Gly Ala Thr Met Gly Leu Ala Thr Leu Arg
100     105     110
Leu Gly Arg Ile Lys Gly Val Glu Arg Pro Ala Ile Cys Thr Leu Met
115     120     125
Pro Ser Val Gly Lys Arg Pro Ser Val Leu Leu Asp Ala Gly Ala Asn
130     135     140
Thr Asp Cys Lys Pro Glu Tyr Leu Ile Asp Phe Ala Leu Met Gly Tyr
145     150     155     160
Glu Tyr Ala Lys Ser Val Leu His Tyr Asp Ser Pro Lys Val Gly Leu
165     170     175
Leu Ser Asn Gly Glu Glu Asp Ile Lys Gly Asn Thr Leu Val Lys Glu
180     185     190
Thr His Lys Met Leu Lys Ala Tyr Asp Phe Phe Tyr Gly Asn Val Glu
195     200     205
Gly Ser Asp Ile Phe Lys Gly Val Val Asp Val Val Val Cys Asp Gly
210     215     220
Phe Met Gly Asn Val Val Leu Lys Thr Thr Glu Gly Val Ala Ser Ala
225     230     235     240
Ile Gly Ser Ile Phe Lys Asp Glu Ile Lys Ser Ser Phe Lys Ser Lys
245     250     255
Met Gly Ala Leu Met Leu Lys Asn Ala Phe Gly Ile Leu Lys Gln Lys
260     265     270
Thr Asp Tyr Ala Glu Tyr Gly Gly Ala Pro Leu Leu Gly Val Asn Lys
275     280     285
Ser Val Ile Ile Ser His Gly Lys Ser Asn Ala Arg Ala Val Glu Cys
290     295     300
Ala Ile Tyr Gln Ala Ile Ser Ala Val Glu Ser Gln Val Cys Leu Arg
305     310     315     320
Ile Thr Gln Ala Phe Glu Ser Leu Lys Ser Gln Ser Phe Glu Ser Gln
325     330     335
Ser Asp Gln Gln Asp Ala
340

```

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

1392

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865

```

Asn Ala His Ala Phe Thr His Pro Phe Ser Ala Pro Ala Arg Phe Arg
1          5          10          15
Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe Leu Arg Pro Asp
          20          25          30
Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn Lys Pro Val Ser
          35          40          45
Val Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro Glu Val Ser Gln
          50          55          60
Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val Tyr Lys Val Leu
65          70          75          80
Pro Lys Glu Tyr Leu His Asp Asn Ile Lys Phe Phe Ile Asn Pro Thr
          85          90          95
Gly Lys Phe Val Ile Gly Gly Pro Gln Gly Asp Ala Gly Leu Thr Gly
          100          105          110
Arg Lys Ile Ile Trp Asp Thr Tyr Gly Gly Phe Cys Pro His Gly Gly
          115          120          125
Gly Ala Phe Thr Gly Lys Asp Pro Tyr Lys Val Asp Met Ser Ala Ala
130          135          140
Tyr Ala Ala Arg Tyr Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys
145          150          155          160
Asp Lys Ala Thr Val Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro
          165          170          175
Val Ser Ile Tyr Val Asn Thr His Asn Thr Ser Lys His Ser Ser Ala
          180          185          190
Glu Leu Glu Lys Cys Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly
          195          200          205
Ile Ile Glu Ser Leu Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser
210          215          220
Ala Tyr Gly His Phe Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys
225          230          235          240
Thr Asn Lys Val Glu Glu Ile Lys Ala Phe Phe Lys Arg
          245          250

```

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866

```

Ser Thr Ile His Lys Glu Phe Lys Leu Lys Gln Arg Thr Leu Ser Ile
1          5          10          15
Ile Lys Pro Asp Ala Leu Lys Lys Lys Val Val Gly Lys Thr Ile Asp
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

1393

```

Arg Phe Glu Ser Asn Gly Leu Glu Val Val Ala Met Lys Arg Leu His
      35              40              45
Leu Ser Val Lys Asp Ala Glu Asn Phe Tyr Ala Ile Leu Arg Glu Arg
      50              55              60
Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro Val Val
      65              70              75              80
Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg Glu Leu
      85              90              95
Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile Arg Ala
      100             105             110
Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser Asp Ser
      115             120             125
Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala Arg Glu
      130             135             140
Phe
145

```

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867

```

Gly Arg Gly Gly Ile Tyr Ile Glu His Gly Arg Val Lys Met Val Ala
1      5      10      15
Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala Gly Tyr Lys
      20      25      30
Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr Val Lys Ile
      35      40      45
Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn Tyr Lys Ser
      50      55      60
Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg Pro Phe Asp
      65      70      75      80
Lys Ala Pro Asn Ile Cys Ile Ala Pro Cys Asp Ala Leu Ile Thr Glu
      85      90      95
Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys Gly Met Pro
      100     105     110
Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu Ser Pro Ser
      115     120     125
Phe Phe Tyr Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr
      130     135     140
His Ala Pro Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly
145     150     155     160
Lys Leu Leu Pro Val Asn Lys Pro Ser Leu His Lys Asn Lys Asn Leu
      165     170     175
Phe Val Gly Asn Glu Arg Val Ala Leu Val Ala Lys Asp Asp Ser Arg
      180     185     190
Gln

```

SUBSTITUTE SHEET (RULE 26)

1394

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868

```

Asn His Asn Lys Gly Ala Glu Ile Ser Leu Trp Gly Leu Thr Arg Leu
1          5          10          15
Val Asp Arg Asp Ile Asp Lys Asp Asn Pro Arg Thr Lys Asn Arg Pro
20          25          30
Ser Val Asp Gly Arg Ile Ser Val Lys Gly Met Val Ile Phe Ser Val
35          40          45
Ser Asn Ala Ile Leu Phe Val Gly Trp Ser Asn Phe Ile Asn Pro Leu
50          55          60
Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile Ile Leu Gly Gly Tyr Ser
65          70          75          80
Tyr Phe Lys Arg Phe Ser Ser Leu Ala His Phe Val Val Gly Leu Ala
85          90          95
Leu Gly Leu Ala Pro Ile Ala Gly Ser Val Ala Val Leu Gly Asp Ile
100          105          110
Pro Leu Trp Asn Val Phe Leu Ala Leu Gly Val Met Leu Trp Val Ala
115          120          125
Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp Met Glu Phe Asp Lys Glu
130          135          140
Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu Gly Glu Lys Trp Cys Leu
145          150          155          160
Asn Leu Ser Arg Leu Ser His Leu Val Ala Leu Ile Cys Trp Leu Cys
165          170          175
Phe Val Lys Cys Tyr His Gly Gly Leu Phe Ala Tyr Leu Gly Leu Gly
180          185          190
Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln Ile Leu Val Ala Arg Asp
195          200          205
Tyr Lys Asn Ile Pro Lys Ala Phe Phe Val Ser Asn Gly Tyr Leu Gly
210          215          220
Val Val Phe Phe Ile Phe Ile Val Leu Asp Val Gly Phe Lys His Ala
225          230          235          240

```

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869

```

Val Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met
1           5           10           15
Trp Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly
20           25           30
Phe Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg
35           40           45
Phe Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp
50           55           60
Trp Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp
65           70           75           80
Thr Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu
85           90           95
Ser Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg
100          105          110
Ile Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu
115          120          125
Ile Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile
130          135          140
Leu Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr
145          150          155          160
Arg Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp
165          170          175
Ser Glu Arg Lys Gly Leu Lys Leu
180

```

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870

```

Thr Gly Ala Ile Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu
1           5           10           15
Gly Ala Ile Leu Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu
20           25           30
Lys Glu Lys Glu Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu
35           40           45
Asp Glu Ser Tyr Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu
50           55           60
Leu Glu Gly Arg Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu
65           70           75           80
Asp Ser Ser Leu Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln

```

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```

      85          90          95
Glu Ile Gln Lys Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys
      100          105          110
Ile Ile Thr
      115

```

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871

```

Glu Pro Ile Lys Ser Asp Lys Glu Ala Phe Asp Leu Val Met Gln Asn
1          5          10          15
Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn Asn Tyr Lys
      20          25          30
Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly Tyr Arg Ile
      35          40          45
Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val Ala Ile Gly
      50          55          60
Leu Glu Leu Gly Glu Asp Pro Gln Val Val Phe Glu Ser Ile Asn
      65          70          75          80
Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg Asn Tyr Leu
      85          90          95
Met Met Gly Glu Asn Ser Asp Asn Gln Asn Arg Leu Tyr Asn Thr Tyr
      100          105          110
Trp Val Pro Leu Glu Asn Trp Leu Gly Glu Lys Asp Leu Asn Asp Phe
      115          120          125
Ile Lys Thr Tyr Leu Arg Ile Tyr Phe Glu Asp Arg Val Lys Glu Gly
      130          135          140
Glu Arg Glu Val Tyr Tyr Ala Leu Lys Ala His His Arg Asp Asn Phe
      145          150          155          160
Pro Asn Asn Ile Gln Gly Leu Met Ser Asp Met Arg Glu Tyr Gly Arg
      165          170          175
Ile Phe Gln Ile Phe Leu Asp Arg Asp His Tyr Phe Leu His Arg Gly
      180          185          190
Asp Pro Gln Gln Leu Ala Asn Leu Arg Leu Arg Val Lys Asp Leu Val
      195          200          205
Lys Ile Lys Phe Gly Val Ala Lys Pro Phe Val Leu Arg Cys Ala Arg
      210          215          220
Asp Phe Glu Glu Gly Lys Leu Asp Tyr Glu Asn Phe His Glu Ile Leu
      225          230          235          240
Gln Ile Leu Ile Ser Tyr Phe Val Arg Arg Ser Val Cys Gly Asp Ser
      245          250          255
Thr Pro Thr Leu Thr Arg Val Leu Tyr Ser Leu Tyr Arg Gln Leu Gly
      260          265          270
Glu Asp Val Ser Ala Asp Ala Leu Lys Arg Tyr Leu Gly Lys Ser Val
      275          280          285
Gly Gln Met Ala Phe Pro Asn Asp Asp Lys Ile Lys Ala Ala Phe Leu
      290          295          300

```

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```

Val Arg Asn Ala Tyr Ala Ala Asn Gln Val Cys Lys Phe Ile Leu Leu
305          310          315          320
Glu Ile Glu Lys Leu Ala Thr Leu Asn Arg Gln Lys Lys Arg Ile
          325          330          335

```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872

```

Phe Tyr Val Ser Ile Ile Lys Cys Thr Pro Leu Leu Val Gln Ile Val
1          5          10          15
Ile Val Phe Tyr Gly Leu Pro Ala Leu Gly Val Tyr Met Asp Pro Ile
          20          25          30
Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val Gly Ala Tyr Ala Ser
          35          40          45
Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro Lys Asp Gln Trp Asp
          50          55          60
Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln Thr Phe Trp His Val
65          70          75          80
Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Ala Lys Pro Lys
          85          90

```

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873

```

Ser Ile Lys His Leu Gly Lys Lys Glu Val Lys Thr Leu Gly Leu Ser
1          5          10          15
Ser Leu Gly Gly Thr Leu Glu Phe Tyr Asp Phe Ile Ile Phe Val Phe
          20          25          30
Phe Thr Ser Ile Ile Ala Lys His Phe Phe Pro Asn Thr Leu Ser Pro

```

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| | | |
|---|-----|-----|
| 35 | 40 | 45 |
| Ile Trp Ser Glu Ile Asn Thr Tyr Gly Ile Phe Ala Ala Gly Tyr Leu | | |
| 50 | 55 | 60 |
| Ala Arg Pro Leu Gly Gly Ile Val Met Ala His Phe Gly Asp Lys Phe | | |
| 65 | 70 | 75 |
| Gly Arg Lys Asn Met Phe Met Leu Ser Ile Leu Leu Met Val Ile Pro | | |
| 85 | 90 | 95 |
| Thr Phe Ala Leu Ala Leu Met Pro Thr Phe Asn Asp Leu Val Gly Phe | | |
| 100 | 105 | 110 |
| Gly Val Asp Ser Met Gly Leu Thr Pro Lys Asn Ala His Tyr Leu Gly | | |
| 115 | 120 | 125 |
| Tyr Ile Ala Pro Val Phe Leu Val Leu Val Arg Ile Cys Gln Gly Val | | |
| 130 | 135 | 140 |
| Ala Val Gly Gly Glu Leu Pro Gly Ala Trp Val Phe Val His Glu His | | |
| 145 | 150 | 155 |
| Ala Pro Gln Gly Gln Lys Asn Thr Tyr Ile Gly Phe Leu Thr Ala Ser | | |
| 165 | 170 | 175 |
| Val Val Ser Gly Ile Leu Leu Gly Ser Leu Val Tyr Ile Gly Ile Tyr | | |
| 180 | 185 | 190 |
| Met Val Phe Asp Lys Pro Val Val Glu Asp Trp Ala Trp Arg Val Ala | | |
| 195 | 200 | 205 |
| Phe Gly Leu Gly Gly Ile Phe Gly Ile Ile Ser Val Tyr Leu Arg Arg | | |
| 210 | 215 | 220 |
| Phe Leu Glu Glu Thr Pro Val Phe Gln Gln Met Lys Gln Asp Asp Ala | | |
| 225 | 230 | 235 |
| Leu Val Lys Phe Pro Leu Lys Glu Val Phe Lys Asn Ser Leu Phe Gly | | |
| 245 | 250 | 255 |
| Ile Ser Ile Ser Met Leu Ile Thr Trp Val Leu Thr Ala Cys Ile Leu | | |
| 260 | 265 | 270 |
| Ile Phe Ile Leu Phe Val Pro Asn Phe Thr Leu Thr His Pro Asn Phe | | |
| 275 | 280 | 285 |
| His Phe Thr Pro Phe Glu Lys Thr Tyr Phe Gln Ile Leu Gly Leu Val | | |
| 290 | 295 | 300 |
| Gly Ile Val Ser Ser Ile Ile Phe Thr Gly Phe Leu Ala Asp Lys Ile | | |
| 305 | 310 | 315 |
| Lys Pro His Lys Val Cys Met Ala Phe Ser Ala Ala Phe Gly Phe Phe | | |
| 325 | 330 | 335 |
| Gly Phe Leu Phe Phe Lys Glu Phe Tyr Ser Asn Ala Pro Ser Leu Val | | |
| 340 | 345 | 350 |
| Asn Thr Ile Ile Leu Tyr Phe Leu Ala Cys Phe Cys Ala Gly Ile Met | | |
| 355 | 360 | 365 |
| Asn Phe Cys Pro Ile Phe Met Ser Asp Val Phe Ser Ala Arg Ile Arg | | |
| 370 | 375 | 380 |
| Phe Ser Gly Ile Ser Phe Ala Tyr Asn Ile Ala Tyr Ala Ile Thr Ala | | |
| 385 | 390 | 395 |
| Gly Phe Thr Pro Gln Leu Ser Ser Trp Leu Asn Ala Lys Ala Ile Ala | | |
| 405 | 410 | 415 |
| Val Pro Glu Ser Leu Gln Ser Tyr Gly Leu Ser Phe Tyr Ile Leu Ile | | |
| 420 | 425 | 430 |
| Val Ser Leu Ile Ala Phe Ile Thr Ser Leu Leu Met Ala Pro Ile Tyr | | |
| 435 | 440 | 445 |
| His Lys Ser Asn Thr Gln His Glu Val Ser Pro Thr Ala | | |
| 450 | 455 | 460 |

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874

```

Lys Ser Leu Lys Lys Lys Cys Arg Ser Phe Leu Gln Glu Tyr Glu Val
1      5      10      15
Tyr Ser Leu Asp Leu Ala Leu Met Val Ala Gly Ala Lys Tyr Arg Gly
      20      25      30
Asp Phe Glu Lys Arg Leu Lys Lys Thr Leu Lys Glu Ile Gln Gln Asn
      35      40      45
Gly Arg Ile Ile Leu Phe Ile Asp Glu Ile His Thr Leu Leu Gly Ala
      50      55      60
Gly Ser Ser Asn Ala Gly Ser Leu Asp Ala Ala Asn Ile Leu Lys Pro
      65      70      75      80
Val Leu Thr Asp Gly Ser Leu Lys Cys Leu Gly Ala Thr Thr Phe Glu
      85      90      95
Glu Tyr Arg Ser Val Phe Glu Lys Asp Lys Ala Phe Asn Arg Arg Phe
      100      105      110
Ser Ile Val Asn Val Glu Glu Pro Ser Lys Glu Ala Cys Tyr Leu Ile
      115      120      125
Leu Lys Asn Ile Ala Pro Leu Tyr Glu Glu His His Gln Val Arg Tyr
      130      135      140
Asn Glu Ser Val Phe Lys Ala Cys Val Asp Leu Thr Ser Tyr Tyr Met
      145      150      155      160
His Asp Lys Phe Leu Pro Asp Lys Ala Ile Glu Leu Leu Asp Glu Val
      165      170      175
Gly Ser Arg Lys Lys Ile Asn Pro Lys Lys Gly Lys Lys Ile Ser Val
      180      185      190
Asp Asp Val Gln Glu Thr Leu Ala Leu Lys Leu Lys Ile Pro Lys Met
      195      200      205
Arg Leu Asn Ser Asp Lys Lys Ala Leu Leu Arg Asn Leu Glu Lys Ser
      210      215      220
Leu Lys Asn Lys Ile Phe Ala Gln Thr Glu Ala Ile Asn Leu Val Ser
      225      230      235      240
Asn Ala Ile Lys Ile Gln His Cys Gly Leu Ser Ala Lys Asn Lys Pro
      245      250      255
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
      260      265      270
Leu Ala Lys Glu Leu Ala Leu Asn Leu Asn Leu His Phe Glu Arg Phe
      275      280      285
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
      290      295      300
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
      305      310      315      320
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
      325      330      335
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Gln Val Met Asp Asn
      340      345      350
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
      355      360      365
Ile Leu Ile Met Thr Ser Asn Val Gly Ser Lys Asp Lys Asp Thr Leu
      370      375      380
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
      385      390      395      400
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
      405      410      415
Asn Ala Leu Ser Leu Glu Asp Phe Glu Arg Ile Val Ser Val Glu Leu
      420      425      430
Asp Gly Leu Lys Ala Leu Ala Ile Glu Gln Gly Val Ile Leu Lys Phe

```

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```

      435              440              445
His Lys Glu Val Val Lys Cys Ile Ala Gln Lys Ser Tyr Gln Arg Ser
  450              455              460
Phe Gly Ala Arg Glu Ile Lys Lys Ile Ile Gln Arg Glu Ile Asn Pro
  465              470              475              480
Gln Leu Ser Asp Ile Val Leu Lys Gln Ser Leu Lys Lys Pro Thr Arg
      485              490              495
Ser Leu Arg Met Lys Ser Thr Phe His Lys Val
      500              505

```

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875

```

Gly Ile Lys Leu Ile Lys Phe Val Arg Asn Val Val Leu Phe Ile Leu
1           5           10           15
Thr Ala Ile Phe Leu Ala Phe Met Leu Leu Val Ser Tyr Cys Met Pro
      20           25           30
His Tyr Ser Val Ala Val Ile Ser Gly Val Glu Val Lys Arg Met Asn
      35           40           45
Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu Val Lys Thr Leu Ala Arg
      50           55           60
Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro Lys Asp Gln Lys Ser Val
      65           70           75           80
Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe Gly Phe Pro Phe Tyr Phe
      85           90           95
Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu Ala Gln Ser Leu Val Asn
      100          105          110
Gln Gln Val Glu Val Gln Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn
      115          120          125
Met Phe Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Asp Glu
      130          135          140
Met Ser Lys Pro Val Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Val
      145          150          155          160
Gly Phe Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Gly Lys
      165          170          175
Ala His

```

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Leu | Leu | Leu | Tyr | Asn | Leu | Lys | Asn | Phe | Ile | Lys | Gly | Lys | Ser |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Ser | Met | Ser | Asn | Gln | Glu | Tyr | Thr | Phe | Gln | Thr | Glu | Ile | Asn | Gln | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Asp | Leu | Met | Ile | His | Ser | Leu | Tyr | Ser | Asn | Lys | Glu | Ile | Phe | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Glu | Leu | Ile | Ser | Asn | Ala | Ser | Asp | Ala | Leu | Asp | Lys | Leu | Asn | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Met | Leu | Thr | Asp | Glu | Lys | Leu | Lys | Gly | Leu | Asn | Thr | Thr | Pro | Ser |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ile | His | Leu | Ser | Phe | Asp | Ser | Gln | Lys | Lys | Thr | Leu | Thr | Ile | Lys | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asn | Gly | Ile | Gly | Met | Asp | Lys | Ser | Asp | Leu | Ile | Glu | His | Leu | Gly | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Ala | Lys | Ser | Gly | Thr | Lys | Ser | Phe | Leu | Ser | Ala | Leu | Ser | Gly | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Lys | Lys | Lys | Asp | Ser | Ala | Leu | Ile | Gly | Gln | Phe | Gly | Val | Gly | Phe | Tyr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ser | Ala | Phe | Met | Val | Ala | Ser | Lys | Ile | Val | Val | Gln | Thr | Lys | Lys | Val |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Thr | Ser | His | Gln | Ala | Tyr | Ala | Trp | Val | Ser | Asp | Gly | Lys | Gly | Lys | Phe |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Glu | Ile | Ser | Glu | Cys | Val | Lys | Glu | Glu | Gln | Gly | Thr | Glu | Ile | Thr | Leu |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Phe | Leu | Lys | Glu | Glu | Asp | Ser | His | Phe | Ala | Ser | Arg | Trp | Glu | Ile | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Val | Val | Lys | Lys | Tyr | Ser | Glu | His | Ile | Pro | Phe | Pro | Ile | Phe | Leu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Tyr | Thr | Asp | Thr | Lys | Phe | Glu | Gly | Glu | Gly | Asp | Asn | Lys | Lys | Glu |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Val | Lys | Glu | Glu | Lys | Cys | Asp | Gln | Ile | Asn | Gln | Ala | Ser | Ala | Leu | Trp |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Lys | Met | Asn | Lys | Ser | Glu | Leu | Lys | Glu | Lys | Asp | Tyr | Lys | Asp | Phe | Tyr |
| | | 260 | | | | | 265 | | | | | 270 | | | |
| Gln | Ser | Phe | Ala | His | Asp | Asn | Ser | Glu | Pro | Leu | Ser | Tyr | Ile | His | Asn |
| | | 275 | | | | 280 | | | | | | 285 | | | |
| Lys | Val | Glu | Gly | Ser | Leu | Glu | Tyr | Thr | Thr | Leu | Phe | Tyr | Ile | Pro | Ser |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Lys | Ala | Pro | Phe | Asp | Leu | Phe | Arg | Val | Asp | Tyr | Lys | Ser | Gly | Val | Lys |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Leu | Tyr | Val | Lys | Arg | Val | Phe | Ile | Thr | Asp | Asp | Asp | Lys | Glu | Leu | Leu |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Pro | Ser | Tyr | Leu | Arg | Phe | Val | Lys | Gly | Val | Ile | Asp | Ser | Glu | Asp | Leu |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Pro | Leu | Asn | Val | Ser | Arg | Glu | Ile | Leu | Gln | Gln | Asn | Lys | Ile | Leu | Ala |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Asn | Ile | Arg | Ser | Ala | Ser | Val | Lys | Lys | Ile | Leu | Ser | Glu | Ile | Glu | Arg |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Leu | Ser | Lys | Asp | Asn | Lys | Asn | Tyr | His | Lys | Phe | Tyr | Glu | Pro | Phe | Gly |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| Lys | Val | Leu | Lys | Glu | Gly | Leu | Tyr | Gly | Asp | Phe | Glu | Asn | Lys | Glu | Lys |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Leu | Leu | Glu | Leu | Leu | Arg | Phe | Tyr | Ser | Lys | Asp | Lys | Gly | Glu | Trp | Ile |

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```

          420          425          430
Ser Leu Lys Glu Tyr Lys Glu Asn Leu Lys Glu Asn Gln Lys Ser Ile
          435          440          445
Tyr Tyr Leu Leu Gly Glu Asn Leu Asp Leu Leu Lys Ala Ser Pro Leu
          450          455          460
Leu Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp
465          470          475          480
Glu Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr
          485          490          495
Pro Phe Arg Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu
          500          505          510
Ala Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Ile Lys
          515          520          525
Ala Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser
530          535          540
Gly His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Pro Asn Ala
545          550          555          560
Met Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser
          565          570          575
Lys Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu
          580          585          590
Leu Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu
          595          600          605
Tyr Asp Gly Ala Lys Leu Leu Glu Lys Gly Ala Leu Lys Asp Ala Lys
610          615          620
Ser Phe Asn Glu Arg Leu Asn Ser Val Leu Leu Lys Ala Leu
625          630          635

```

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877

```

Lys Gln Phe Gly Arg Arg Val Phe Thr Gln Ile Pro Lys Met Val Gln
1          5          10          15
Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe Lys Asn Ala
          20          25          30
Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr Lys Glu Asn
          35          40          45
Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln Glu Asp Val
50          55          60
Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu Lys Asp Ile
65          70          75          80
Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp Asn Gln Leu
          85          90          95
Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr Ser Ala Ile
100          105          110
Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly Val Lys Ala
115          120          125

```

SUBSTITUTE SHEET (RULE 26)

1403

```

Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala Pro Lys Pro
130      135      140
Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val Met Ile Ser
145      150      155      160
Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val Asn Leu Ser
      165      170      175
Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu Asp Ala Asp
      180      185      190
Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln Asn Ala Asp
      195      200      205
Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu Lys Ala Phe
      210      215      220
Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu Gly Gln Ser
225      230      235      240
Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu Gln Met Leu
      245      250      255
Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val Asp Met Pro
      260      265      270
Pro Gly Thr Gly Asp Ala Gln Leu Thr Leu Ala Gln Ala Val Pro Leu
      275      280      285
Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser Leu Asp Asp
      290      295      300
Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile Pro Ile Ala
305      310      315      320
Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His Cys Lys Lys
      325      330      335
Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu Leu Glu Ala
      340      345      350
Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro Lys Val Arg
      355      360      365
Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His Pro Thr Ser
      370      375      380
Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu Ser Ala Phe
385      390      395      400
Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys Asp Ile Gln
      405      410      415
Pro Thr Gln Thr His Ala Tyr Ser His
      420      425

```

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878

```

Leu Gly Phe Leu Ala Leu His Gly Phe Phe Leu Ser Ala Phe Glu Tyr
1      5      10      15
Gln Val Ser Ala Arg Val Gly Ser Phe Ser Arg Ile Ala Phe Asn Gln
      20      25      30
Ser Ile Ile Asn Ser Lys Lys Gly Ile Tyr Pro Thr Gly Ser Tyr Val

```

SUBSTITUTE SHEET (RULE 26)

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Thr | Thr | Gly | Ala | Leu | Gln | Val | Asp | Ser | Ser | Leu | Leu | Pro | Lys | Gly | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ile | Glu | Asn | His | Lys | Leu | Gly | Phe | Gly | Val | Gly | Gly | Glu | Ile | Gly | Ala | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Ala | Tyr | Asp | Ser | Thr | Lys | Phe | Leu | Ile | Asp | Glu | Ala | Asn | Pro | Lys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Gly | Phe | Gln | Pro | Ala | Asn | Trp | Tyr | Tyr | Met | Gly | Arg | Trp | Glu | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Tyr | Leu | Met | Gln | His | Ser | Gln | Asn | Trp | Thr | Arg | Glu | Gln | Lys | Ala | Gln | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Ala | Arg | Pro | Tyr | Val | Leu | Tyr | Asn | Leu | Tyr | Leu | Asp | Tyr | Gln | Tyr | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Lys | Asp | Ile | Phe | Gly | Ile | Lys | Leu | Gly | Arg | Tyr | Pro | Ser | Lys | Ala | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Phe | Leu | Ser | Gly | Phe | Asn | Gln | Gly | Phe | Glu | Ile | Phe | Tyr | Arg | Trp | Lys | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Lys | Phe | Lys | Ile | Val | Trp | Phe | Ser | Thr | Phe | Gly | Arg | Ala | Leu | Ala | Asn | |
| | | | 180 | | | | | 185 | | | | 190 | | | | |
| Glu | Gln | Tyr | Ile | Arg | Asp | Phe | Tyr | Ala | Pro | Val | Asn | Tyr | Lys | Gln | Lys | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ile | Asn | Tyr | Gly | Met | His | Asn | Phe | Asn | Leu | Val | Tyr | Glu | Asn | Lys | Tyr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Ile | Arg | Ile | Ala | Pro | Phe | Ile | Trp | Phe | Tyr | Pro | Lys | Asn | Phe | Asn | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Pro | Gly | Phe | Glu | Ile | Thr | His | Asp | Thr | Lys | Ser | Tyr | Trp | Lys | Ser | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Trp | Arg | Ile | Gln | Thr | Thr | Phe | Tyr | Ala | Trp | Phe | Pro | Leu | Tyr | Ser | Asp | |
| | | | 260 | | | | | 265 | | | | 270 | | | | |
| Tyr | Leu | Ser | Lys | Asp | Tyr | Tyr | Arg | Ala | Ala | Leu | Val | Gly | Lys | Lys | Ser | |
| | | 275 | | | | | 280 | | | | 285 | | | | | |
| Ala | Ala | Leu | Phe | Val | Phe | Gln | Arg | Val | Asn | Phe | Arg | Ser | Tyr | Arg | Phe | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| Gly | Trp | Ser | Val | Tyr | Lys | Asn | Gly | Asn | Ala | Ser | Val | Gln | Leu | Gly | | |
| 305 | | | | | 310 | | | | 315 | | | | | 320 | | |
| Trp | Asn | Gly | Ser | Pro | Ile | Asp | Pro | Phe | Tyr | Asp | Thr | Lys | Asp | Asp | Thr | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Pro | Tyr | Glu | Asp | Ala | Tyr | Ser | Asn | Phe | Tyr | Asn | Ala | Asn | Ser | Ile | Thr | |
| | | 340 | | | | | | 345 | | | | 350 | | | | |
| Ile | Asn | Ala | Phe | Ile | Gly | Lys | Ser | Ile | Lys | Asn | Leu | Leu | Val | Gln | Leu | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Tyr | Gly | Lys | Leu | Thr | Tyr | Ser | Pro | Arg | Ala | Asp | Ala | Gln | Ser | Leu | Gly | |
| | 370 | | | | | 375 | | </ | | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

1405

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879

```

Tyr Pro Thr Asn Thr Ile Ile Glu Arg Ile Leu Met Phe Lys Lys Met
1      5      10      15
Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys Val Gly Ala Lys Asp
20      25      30
Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly Gly Lys Phe Met Gly
35      40      45
Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr Ser Met Asn Asp Glu
50      55      60
Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg Gly Asn Ser Val Glu
65      70      75      80
Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp Lys Phe Lys Lys Glu
85      90      95
Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln Gln Ile Phe Tyr Arg
100     105     110
Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val Lys Ile Ile Thr Asp
115     120     125
Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
130     135

```

(2) INFORMATION FOR SEQ ID NO:1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880

```

Arg Ile Gly Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr
1      5      10      15
Pro Thr Ile Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser
20      25      30
Leu Phe Pro Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys
35      40      45
Asn Leu Phe Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu
50      55      60
Lys Glu His Ala Lys Glu Lys His Val Lys Glu Asn Val Lys Pro Leu
65      70      75      80
His Phe Cys Phe Ala Gly His Ile Asp Val Val Pro Pro Gly Asn Asn
85      90      95
Trp Gln Ser Asp Pro Phe Lys Pro Ile Ile Lys Glu Gly Phe Leu Tyr
100     105     110
Gly Arg Gly Ala Gln Asp Met Lys Gly Gly Val Gly Ala Phe Leu Ser
115     120     125
Ala Ser Leu Asn Phe Asn Pro Lys Thr Pro Phe Leu Leu Ser Ile Leu

```

SUBSTITUTE SHEET (RULE 26)

1406

```

130          135          140
Leu Thr Ser Asp Glu Glu Gly Pro Gly Ile Phe Gly Thr Arg Leu Met
145          150          155          160
Leu Glu Lys Leu Lys Glu Lys Asp Leu Leu Pro His Met Ala Ile Val
          165          170          175
Ala Glu Pro Thr Cys Glu Lys Val Leu Gly Asp Ser Ile Lys Ile Gly
          180          185          190
Arg Arg Gly Ser Ile Asn Gly Lys Leu Ile Leu Lys Gly Val Gln Gly
          195          200          205
His Val Ala Tyr Pro Gln Lys Cys Gln Asn Pro Ile Asp Thr Leu Ala
          210          215          220
Ser Val Leu Pro Leu Ile Ser Gly Val His Leu Asp Asn Gly Asp Glu
225          230          235          240
Cys Phe Asp Pro Ser Lys Leu Val Ile Thr Asn Leu His Ala Gly Leu
          245          250          255
Gly Ala Asn Asn Val Thr Pro Gly Ser Val Glu Ile Ala Phe Asn Ala
          260          265          270
Arg His Ser Leu Lys Thr Thr Gln Glu Ser Leu Lys Glu Tyr Leu Glu
          275          280          285
Lys Val Leu Lys Asp Leu Pro Tyr Thr Leu Glu Leu Glu Ser Ser Ser
290          295          300
Ser Pro Phe Ile Thr Ala Ser His Ser Lys Leu Thr Ser Val Leu Gln
305          310          315          320
Glu Asn Ile Leu Lys Thr Cys His Thr Thr Pro Leu Leu Asn Thr Lys
          325          330          335
Gly Gly Thr Ser Asp Ala Arg Phe Phe Ser Ala His Gly Ile Glu Val
          340          345          350
Val Glu Phe Gly Ala Ile Asn Asp Arg Ile His Ala Val Asp Glu Arg
          355          360          365
Val Ser Leu Lys Glu Leu Glu Leu Glu Lys Val Phe Leu Gly Val
370          375          380
Leu Glu Gly Leu Ser Glu Lys
385          390

```

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881

```

Thr Ser Leu Asp His Lys Ile Thr Asp Phe Ser Cys Val Asp Leu Arg
1          5          10          15
Ile Gln Ser Lys Glu Val Ser His Asn Leu Lys Glu Leu Ser Lys Thr
20          25          30
Leu Ile Ser Tyr Pro Phe Glu Lys His Val Glu Ala Leu Gly Glu Gln
35          40          45
Cys Ser Asn Phe Val Ser Ile Pro Ile Asn Asn Asp Asp Tyr Ser Asn
50          55          60
Ile Cys Thr Phe Val Ser Asp Phe Ile Asn Leu Ile Ala Ser Tyr Asn
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

1407

Leu Leu Glu Ser Phe Leu Asp Phe Tyr Lys Asp Lys Leu Lys Leu Ser
 85 90 95
 Glu Leu Val Thr Glu Tyr Ala Asn Val Thr Asn Asn Leu Leu Phe Lys
 100 105 110
 Lys Leu Ile Lys His Leu Ser Gly Asn Asn Gln Leu Val Lys Asn Phe
 115 120 125
 Tyr Gln Cys Ile Arg Glu Ile Ile Lys Tyr Asn Ala Pro Asn Lys Glu
 130 135 140
 Tyr Lys Pro Asn Gln Phe Phe Ile Ile Gly Lys Gly Lys Gln Lys Gln
 145 150 155 160
 Leu Ala Lys Ile Tyr Ser His Leu Lys Glu Leu Ser Ala Ser Glu Ile
 165 170 175
 Lys Pro Gln Asp Met Glu Asp Ile Leu Lys Lys Leu Glu Glu Leu Asp
 180 185 190
 Lys Ile Phe Lys Thr Thr Asp Phe Thr Lys Phe Thr Pro Lys Thr Glu
 195 200 205
 Ile Lys Asp Ile Ile Lys Glu Ile Asp Glu Lys Tyr Pro Ile Asn Glu
 210 215 220
 Asn Phe Lys Arg Gln Phe Asn Glu Phe Glu Ser Asn Ile Glu Lys His
 225 230 235 240
 Asp Glu Ile Lys Lys Asp Phe Glu Arg Asn Lys Glu Ser Leu Ile Arg
 245 250 255
 Glu Ile Glu Asn His Cys Lys Asn Glu Cys Asn Ser Glu Glu Glu Pro
 260 265 270
 Glu Tyr Lys Ile Asn Asp Leu Leu Lys Asn Ile Gln Gln Ile Cys Lys
 275 280 285
 Asn Tyr Ile Glu Ser His Ala Val Asn Asp Val Ser Lys Asp Ile Lys
 290 295 300
 Ser Met Met Cys Gln Phe Tyr Leu Lys Gln Ile Asp Leu Leu Val Asn
 305 310 315 320
 Ser Glu Ile Val Arg Tyr Arg Tyr Ser Asn Leu Phe Glu Pro Ile Gln
 325 330 335
 Arg Ser Leu Trp Glu Ser Ile Lys Ile Leu Asp Asn Glu Ser Gly Ile
 340 345 350
 Tyr Leu Phe Pro Lys Asn Ile Gly Glu Ile Lys Asp Lys Phe Glu Ala
 355 360 365
 Asn Lys Glu Lys Phe Lys Gln Ser Lys Asn Val Ser Glu Phe Ala Glu
 370 375 380
 Tyr Cys Arg Glu Cys Asn Pro Tyr Thr Ala Phe Asn Phe His Leu Asn
 385 390 395 400
 Ile Asn Asn Gly Leu Ser His Gln Phe Glu Lys Phe Val Pro Ile Met
 405 410 415
 Lys Glu Tyr Lys Glu Pro Lys Ile Thr Asp Asn Asp Leu Glu Ala Ile
 420 425 430
 Ser Thr Lys Glu Thr Gly Leu Ala Ser Gln Leu Ser Gly His Trp Phe
 435 440 445
 Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn Phe Asn Pro Asn Lys Ile
 450 455 460
 Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser Lys Ile Lys Phe Asp Lys
 465 470 475 480
 Asp Leu Glu Ile Tyr Phe Asp Ser His Glu Ser Phe Asn Ile Ser Lys
 485 490 495
 Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser Leu Lys Lys Ile Lys Gln
 500 505 510
 Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile Glu Ser Lys His Asp Asn
 515 520 525
 Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu Asn Asp Thr Ser Phe Leu
 530 535 540
 Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu Glu Tyr Asn Met Gln Leu
 545 550 555 560
 Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe Asn Lys Leu Leu Ala Ile
 565 570 575
 Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln Leu Lys Ile Arg Val Arg
 580 585 590
 His Asn Asn Lys Leu Pro Arg Glu Lys Tyr Thr Glu His Glu Ile Lys

SUBSTITUTE SHEET (RULE 26)

1408

```

      595      600      605
Leu Glu Val Tyr Asp Cys Arg Lys Ser His Asp His Asn Glu Pro Ile
  610      615      620
Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln Trp Ala Phe Asn Phe Met
625      630      635      640
Phe Gly Phe Leu Tyr Asn Val Gly Ser His Phe Ser Phe Asn His Asn
      645      650      655
Ile Ile Tyr Val Met Asp Glu Pro Ala Thr His Leu Ser Val Pro Ala
  660      665      670
Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu Tyr Ala His Lys Asn His
  675      680      685
Val Thr Phe Val Leu Ala Thr His Asp Pro Phe Leu Val Asp Thr Asp
  690      695      700
His Leu Asp Glu Ile Arg Ile Val Glu Lys Glu Thr Glu Gly Ser Val
705      710      715      720
Ile Lys Asn His Phe Asn Tyr Pro Leu Asn Asn Ala Ser Lys Asp Ser
      725      730      735
Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu Gly Val Gly Gln His Val
  740      745      750
Phe His Asn Pro Gln Lys His Arg Ile Ile Phe Val Glu Gly Ile Thr
  755      760      765
Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu Tyr Leu Arg Tyr Lys Glu
  770      775      780
Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe Leu Pro Ile Ser Gly Leu
785      790      795      800
Lys Asn Asp Ser Asn Asp Met Lys Glu Thr Ile Glu Lys Leu Cys Glu
      805      810      815
Leu Asp Asn His Pro Ile Val Leu Thr Asp Asp Asp Arg Lys Cys Val
  820      825      830
Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe Lys Arg Ala Asn Glu Glu
  835      840      845
Met His Asp Pro Ile Thr Ile Leu Gln Leu Ser Asp Cys Asp Arg His
  850      855      860
Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala Asn Asp Arg Asn Lys Tyr
865      870      875      880
Ala Lys Asn Lys Gln Met Glu Leu Ser Met Ala Phe Lys Thr Arg Leu
      885      890      895
Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys Gln Thr Lys Arg Asn Phe
  900      905      910
Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala Thr Asn Leu Ile Lys Asn
  915      920      925

```

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882

```

Gln Ala Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile
1           5           10           15

```

SUBSTITUTE SHEET (RULE 26)

1409

```

Leu Cys Phe Gly Phe Ile Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr
      20      25      30
Lys Glu Asn Met Thr Glu Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys
      35      40      45
Asp Ala Pro Ile Leu Leu Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu
      50      55      60
Lys Glu Glu Asn Glu Val Ala Lys Lys Ile Asp Glu Lys Ser Leu Leu
      65      70      75      80
Glu Glu Ile His Lys Lys Lys Arg Gln Leu Tyr Met Leu Lys Gly Glu
      85      90      95
Leu His Glu Lys Asn Glu Ser Ile Leu Phe Gln Gln Met Ala Lys Asn
      100      105      110
Lys Ser Gly Phe Phe Ile Gly Val Ile Leu Gly Asp Ile Gly Ile Asn
      115      120      125
Ala Asn Pro Tyr Glu Lys Phe Glu Leu Leu Ser Asn Ile Gln Ala Ser
      130      135      140
Pro Leu Leu Tyr Gly Leu Arg Ser Gly Tyr Gln Lys Tyr Phe Ala Asn
      145      150      155      160
Gly Ile Ser Ala Leu Arg Phe Tyr Gly Glu Tyr Leu Gly Gly Ala Met
      165      170      175
Lys Gly Phe Lys Ser Asp Ser Leu Ala Ser Tyr Gln Thr Ala Ser Leu
      180      185      190
Asn Ile Asp Leu Leu Met Asp Lys Pro Ile Asp Lys Glu Lys Arg Phe
      195      200      205
Ala Leu Gly Ile Phe Gly Gly Val Gly Val Gly Trp Asn Gly Met Tyr
      210      215      220
Gln Asn Leu Lys Glu Ile Arg Gly Tyr Ser Gln Pro Asn Ala Phe Gly
      225      230      235      240
Leu Val Leu Asn Leu Gly Val Ser Met Thr Leu Asn Leu Lys His Arg
      245      250      255
Phe Glu Leu Ala Leu Lys Met Pro Pro Leu Lys Glu Thr Ser Gln Thr
      260      265      270
Phe Leu Tyr Tyr Phe Lys Ser Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn
      275      280      285
Tyr Leu Leu
      290

```

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883

```

Arg Phe Phe Arg Lys His Arg Val Ile Ser Met Lys Glu Ile Val Thr
1      5      10      15
Ile Glu Asn Val Ser Phe Asn Tyr His Asn Arg Ala Ile Phe Lys Asp
      20      25      30
Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe Leu Cys Val Leu Gly Glu
      35      40      45
Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly Leu Ile Leu Gly Leu Leu

```

SUBSTITUTE SHEET (RULE 26)

1410

```

      50              55              60
Lys Pro Ser Leu Gly Ser Val Lys Ile Phe Asn Glu Thr Leu Ser Asn
65              70              75              80
Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr Ile Ala Gln Gly Asn Ser
      85              90              95
Leu Phe Pro His Leu Asn Ala Leu Gln Asn Met Thr Phe Cys Leu Asn
      100              105              110
Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln Lys Glu Ala Lys Ala Leu
      115              120              125
Ala Leu Lys Met Gly Leu Asp Glu Ser Leu Met Asp Lys Phe Pro Asn
      130              135              140
Glu Leu Ser Gly Gly Gln Ala Gln Arg Val Gly Ile Ile Arg Gly Ile
145              150              155              160
Ile His Arg Pro Glu Leu Ile Leu Leu Asp Glu Pro Phe Ser Ala Leu
      165              170              175
Asp Ser Leu Asn Arg Lys Asn Leu Gln Asp Leu Ile Lys Glu Ile His
      180              185              190
Gln Asn Ser Cys Ala Thr Phe Ile Met Val Thr His Asp Glu Asn Glu
      195              200              205
Ala Gln Lys Leu Ala Thr Lys Thr Leu Glu Ile Lys Ala Leu Lys Gln
      210              215              220
Glu Gln
225

```

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884

```

Met Ala Asp Leu Leu Ser Ser Leu Lys Asn Leu Ser Ser Ser Ser Gly
1              5              10              15
Val Tyr Gln Tyr Phe Asp Lys Asn Arg Gln Leu Leu Tyr Ile Gly Lys
      20              25              30
Ala Lys Asn Leu Lys Lys Arg Ile Lys Ser Tyr Phe Ser Val Arg Asn
      35              40              45
Asn Glu Ile Thr Pro Asn Pro Arg Thr Ser Leu Arg Val Gln Met Met
      50              55              60
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
65              70              75              80
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
      85              90              95
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
      100              105              110
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
      115              120              125
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
      130              135              140
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
145              150              155              160

```

SUBSTITUTE SHEET (RULE 26)

1411

```

Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
      165      170      175
Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
      180      185      190
Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
      195      200      205
Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
      210      215      220
Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
      225      230      235      240
Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
      245      250      255
Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
      260      265      270
Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
      275      280      285
Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
      290      295      300
His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
      305      310      315      320
Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
      325      330      335
Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
      340      345      350
Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
      355      360      365
Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
      370      375      380
Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
      385      390      395      400
Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
      405      410      415
Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
      420      425      430
Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
      435      440      445
Asp Phe Ala Lys Glu Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
      450      455      460
Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
      465      470      475      480
Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Asp Ser Lys Ala
      485      490      495
Tyr Arg Ser Lys Gly Gly Ala Lys Asp Ile Ile His Thr Ile Ser His
      500      505      510
Thr Phe Lys Leu Leu Pro Ser Asp Lys Arg Leu Gln Trp Val Gln Lys
      515      520      525
Leu Arg Asp Glu Ser His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr
      530      535      540
Lys Leu Lys Asn Met Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile
      545      550      555      560
Gly Glu Ala Ser Val Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu
      565      570      575
Ala Ile Glu Lys Ala Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys
      580      585      590
Arg Lys

```

(2) INFORMATION FOR SEQ ID NO:1885:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885

```

Arg Lys Asn Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Gly
1      5      10      15
Cys Val Gly Ser Thr Val Ala Lys Ile Leu Gln Glu Asn Gln Glu Ile
20      25      30
Ile Lys Asp Arg Ala Gly Val Glu Ile Lys Ile Lys Lys Ala Val Val
35      40      45
Arg Asp Val Lys Lys His Lys Gly Tyr Ala Phe Glu Ile Ser Asp Asp
50      55      60
Leu Glu Ser Val Ile Glu Asp Lys Gly Ile Asp Ile Val Val Glu Leu
65      70      75      80
Met Gly Gly Val Glu Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala
85      90      95
Lys Gln Lys Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His
100     105     110
Arg Tyr Glu Leu Glu Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Glu
115     120     125
Ala Ser Val Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly
130     135     140
Leu Ser Ala Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr
145     150     155     160
Ser Asn Tyr Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys
165     170     175
Asp Ala Leu Lys Asp Ala Gln His Leu Gly Tyr Ala Glu Leu Asn Pro
180     185     190
Glu Phe Asp Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu
195     200     205
Ala Ser Leu Ala Tyr Gly Ile Asp Ala Lys Leu Glu Glu Ile Leu Ile
210     215     220
Glu Gly Ile Glu Lys Ile Glu Pro Asp Asp Met Glu Phe Ala Lys Glu
225     230     235     240
Phe Gly Tyr Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Asp
245     250     255
Cys Ile Glu Leu Arg Val His Pro Ser Met Ile Lys Asn Glu Cys Met
260     265     270
Leu Ser Lys Val Asp Gly Val Met Asn Ala Ile Ser Val Ile Gly Asp
275     280     285
Lys Val Gly Glu Thr Leu Tyr Tyr Gly Ala Gly Ala Gly Gly Glu Pro
290     295     300
Thr Ala Ser Ala Val Ile Ser Asp Ile Ile Glu Ile Ala Arg Lys Lys
305     310     315     320
Ser Ser Leu Met Leu Gly Phe Glu Thr Pro Gln Lys Leu Pro Leu Lys
325     330     335
Pro Lys Glu Glu Ile Gln Cys Ala Tyr Tyr Ala Arg Leu Leu Val Ser
340     345     350
Asp Glu Lys Gly Val Phe Ser Gln Ile Ser Ala Ile Leu Ala Gln Asn
355     360     365
Asp Ile Ser Leu Asn Asn Val Leu Gln Lys Glu Ile Pro Gln Ser Asn
370     375     380
Lys Ala Lys Ile Leu Phe Ser Thr His Thr Thr Asn Glu Lys Ser Met
385     390     395     400
Leu Asn Ala Leu Lys Glu Leu Glu Asn Leu Gln Ser Val Leu Asp Thr
405     410     415

```

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Pro Lys Met Ile Arg Leu Glu Asn
420

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886

```

Ser Arg Phe Lys Arg Ala Ile Glu Gln Ala Phe Arg Leu Val Ala Met
1      5      10      15
Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala Gly
20      25      30
Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu Phe Glu Lys
35      40      45
Gly Met Pro Gly Gly Gln Ile Thr Gly Ser Ser Glu Ile Glu Asn Tyr
50      55      60
Pro Gly Val Lys Glu Val Val Ser Gly Leu Asp Phe Met Gln Pro Trp
65      70      75      80
Gln Glu Gln Cys Phe Arg Phe Gly Leu Lys His Glu Met Thr Ala Ile
85      90      95
Gln Arg Val Ser Lys Lys Gly Ser His Phe Val Ile Leu Ala Glu Asp
100     105     110
Gly Lys Thr Phe Glu Ala Lys Ser Val Ile Ile Ala Thr Gly Gly Ser
115     120     125
Pro Lys Arg Thr Gly Ile Lys Gly Glu Ser Glu Tyr Trp Gly Lys Gly
130     135     140
Val Ser Thr Cys Ala Thr Cys Asp Gly Phe Phe Tyr Lys Asn Lys Glu
145     150     155     160
Val Ala Val Leu Gly Gly Gly Asp Thr Ala Val Glu Glu Ala Ile Tyr
165     170     175
Leu Ala Asn Ile Cys Lys Lys Val Tyr Leu Ile His Arg Arg Asp Gly
180     185     190
Phe Arg Cys Ala Pro Ile Thr Leu Glu His Ala Lys Asn Asn Ser Lys
195     200     205
Ile Glu Phe Leu Thr Pro Tyr Val Val Glu Glu Ile Lys Gly Asp Ala
210     215     220
Ser Gly Val Ser Ser Leu Ser Ile Lys Asn Thr Ala Thr Asn Glu Lys
225     230     235     240
Arg Glu Leu Val Val Pro Gly Leu Phe Ile Phe Val Gly Tyr Asp Val
245     250     255
Asn Asn Ala Val Leu Lys Gln Glu Asp Asn Ser Met Leu Cys Glu Cys
260     265     270
Asp Glu Tyr Gly Ser Ile Val Val Asp Phe Ser Met Lys Thr Asn Val
275     280     285
Gln Gly Leu Phe Ala Ala Gly Asp Ile Arg Ile Phe Ala Pro Lys Gln
290     295     300
Val Val Cys Ala Ala Ser Asp Gly Ala Thr Ala Ala Leu Ser Val Ile
305     310     315     320
Ser Tyr Leu Glu His His

```

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(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887

```

Lys Leu Trp Glu Phe Ser Leu Arg Val Phe Ile Ile Ser Leu Asn Gln
1      5      10      15
Lys Val Cys Asp Lys Phe Gly Leu Val Phe Arg Asp Thr Thr Thr Leu
20      25      30
Leu Asn Asn Ile Asn Ala Thr His Gln Ala Gln Ile Phe Asp Ala
35      40      45
Ile Tyr Ser Lys Thr Phe Glu Gly Gly Leu His Pro Leu Val Lys Lys
50      55      60
His Leu His Pro Tyr Phe Ile Thr Gln Asn Ile Lys Asp Met Gly Ile
65      70      75      80
Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr Ala Leu Lys
85      90      95
Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys Tyr Ala Ser
100     105     110
His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu Ala Ile Cys
115     120     125
Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys Glu Gly Leu
130     135     140
Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala Arg Leu Met
145     150     155     160
His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro Leu Asn His Glu
165     170     175
Asn Gln Glu Ile Gln Glu Arg Val Gly Ile Ile Lys Ala Tyr Ser His
180     185     190
Gly Val Gly Thr Gln Gly Tyr Val Ile Thr Pro Lys Ile Ala Lys Val
195     200     205
Phe Leu Lys His Ser Arg Lys Trp Val Val Pro Val Asp Thr Ile Met
210     215     220
Asp Ala Thr Phe Ile His Gly Val Lys Asn Leu Val Leu Gln Pro Phe
225     230     235     240
Val Ile Ala Asp Asp Glu Gln Ile Ser Thr Ile Ala Arg Lys Glu Glu
245     250     255
Pro Tyr Ser Pro Lys Ile Ala Leu Met Arg Glu Leu His Phe Lys Phe
260     265     270
Leu Lys Trp Trp Gln Phe Val
275

```

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888

```

Gly Asp Phe Ile Ile Ser Asn Ile Ser Ile His Pro Lys Thr Met Phe
1          5          10          15
Lys Asn Ala Leu Asn Ile Gln Asp Phe Ser Phe Lys Asn His Thr Ser
20          25          30
Thr Ala Ile Ile Gly Thr Asn Gly Ala Gly Lys Ser Thr Leu Ile Asn
35          40          45
Thr Ile Leu Gly Ile Arg Ser Asp Tyr Asn Phe Lys Ala Gln Asn Asn
50          55          60
Asn Ile Pro Tyr His Asp Asn Val Ile Pro Gln Arg Lys Gln Leu Gly
65          70          75          80
Val Val Ser Asn Leu Phe Asn Tyr Pro Pro Gly Leu Asn Ala Asn Asp
85          90          95
Leu Phe Lys Phe Tyr Gln Phe Phe His Lys Asn Cys Thr Leu Asp Leu
100         105         110
Phe Glu Lys Asn Leu Leu Asn Lys Thr Tyr Glu His Leu Ser Asp Gly
115         120         125
Gln Lys Gln Arg Leu Lys Ile Asp Leu Ala Leu Ser His His Pro Gln
130         135         140
Leu Val Ile Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu
145         150         155         160
Ile Arg Leu Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr
165         170         175
Ser Ile Ile Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp
180         185         190
Val Leu Leu Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn
195         200         205
Ser Ile Leu Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro
210         215         220
Thr Thr Lys Asp Leu Leu Ala Leu Leu Lys Asp Ile
225         230         235

```

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...113

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889

```

Ile Tyr Ser His Leu Ala Pro Ile Met His Tyr Gln Leu Thr Ser Phe
1           5           10           15
Asn Ile Ile Gln Asp Leu Phe Ile Thr Cys His Val Leu Arg Ile Lys
20           25           30
Met Arg Val Phe Val Cys Phe Leu Gly Val Phe Val Ser Asn Gly Leu
35           40           45
Ala Arg Phe Gly Tyr Val Val Leu Ile Pro Leu Leu Ile Leu Ser Gly
50           55           60
Ser Leu Thr Pro His Gln Ser Phe Gln Leu Gly Ile Ala Val Leu Met
65           70           75           80
Gly Tyr Val Phe Gly Ser Phe Leu Ile Gln Phe Leu Ser Pro Leu Met
85           90           95
Ser Leu Glu Ser Ile Ala Lys Ile Ser Phe Lys Leu Ile Thr Leu Ser
100          105          110
Phe

```

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890

```

Ser Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu
1           5           10           15
Val Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys
20           25           30
Gly Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp
35           40           45
Glu Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr
50           55           60
Gln Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891

```

Arg Lys Thr Asn His Lys Arg Leu Ile Ser Val Thr Lys Gly Tyr Leu
1      5      10      15
Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu
20      25      30
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met
35      40      45
Leu Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe
50      55      60
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser
65      70      75      80
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn
85      90      95
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr
100     105     110
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
115     120     125
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
130     135     140
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
145     150     155     160
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
165     170     175
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
180     185     190
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
195     200     205
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
210     215     220
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
225     230     235     240
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
245     250     255
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
260     265

```

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892

Arg Lys Gln Glu Met Lys Lys Leu Leu Leu Leu Glu His Lys Ile

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```

1           5           10           15
Val Lys Ile Gly Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu
      20           25           30
Phe Tyr Glu Gln Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly
      35           40           45
Lys Phe Pro Thr Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys
      50           55           60
Asn Lys Ile Asp Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys
      65           70           75           80
Ser Val Asn Glu Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe
      85           90           95
Asn Ala Leu Val Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys
      100          105          110
Thr Leu Ile Lys Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn
      115          120          125
Glu Asp Glu Lys Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser
      130          135          140
Gln Lys Glu Thr Gln Pro Pro Ile Ser Ile Lys Asn Ser Val Ser His
      145          150          155          160
Ile Lys Ser Lys Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro
      165          170          175
Ser Val Ser Phe Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Ser Phe
      180          185          190
Ser Ser Phe Glu Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys
      195          200          205
Glu Lys Leu Lys Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser
      210          215          220
Leu Leu Ser Ser Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu
      225          230          235          240
Ile Gly Leu Ile Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn
      245          250          255
Ala Ser Asn Asn Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
      260          265          270

```

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893

```

Lys Ile Phe Lys Lys Ala Leu Arg His Lys Met Glu Lys Val Cys Val
1           5           10           15
Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu Glu Arg Leu Lys Glu Lys
      20           25           30
Tyr Gly Asp Asp Trp Glu Lys His Val Lys Ala Lys Ala Ile Asn Glu
      35           40           45
Glu Glu Leu Glu Glu Gln Val Lys Ala Lys Ala Lys Glu Gln Gln Lys
      50           55           60
Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe Leu Lys Lys Val Gly Leu
      65           70           75           80

```

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Lys Lys Arg Asp Met Leu Gln Ser Thr Met Leu Phe Asp Glu Val Lys
 85 90 95
 Glu Ala Asp Val Leu Phe Gln Ala Glu Arg Lys Ile Gly Asp Trp Ile
 100 105 110
 Phe Ser Ser Ala Val Phe Phe Phe Ala Leu Ala Leu Ile Glu Ala Ile
 115 120 125
 Ile Ile Val Cys Leu Leu Pro Leu Lys Glu Lys Val Pro Tyr Leu Val
 130 135 140
 Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala Ile Val Gln Arg Ala Asp
 145 150 155 160
 Lys Ser Ile Arg Ala Asn Gln Ala Leu Val Arg Gln Leu Val Ala Ser
 165 170 175
 Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser Ile Lys Glu Gln Asn Glu
 180 185 190
 Ile Ala His Glu Thr Ile Arg Leu Gln Ser Ala Phe Glu Val Trp Asp
 195 200 205
 Phe Phe Glu Lys Leu Val Ser Tyr Glu His Ser Ile Tyr Thr Asn Ile
 210 215 220
 Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn Ile Ala Leu Ile Ser Lys
 225 230 235 240
 Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln Leu Phe His Lys Glu Lys
 245 250 255
 Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile Met Thr Phe Glu Phe Glu
 260 265 270
 Pro Ile Glu Ile Asp Thr Lys Ser Val Pro Leu Asn Pro Thr Gly Phe
 275 280 285
 Ile Val Thr Gly Tyr Asp Val Thr Glu Ile Ala Ile Leu Lys Asp Leu
 290 295 300
 Asp Glu Lys Asn Lys Val Lys Asp Asp Gly Val Lys Ser Arg Ile Ile
 305 310 315 320
 His Val Glu Lys Lys Asp Pro His Met Ser Gln Tyr Lys Asp Val Lys
 325 330 335
 Glu Gln

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894

Val Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser
 1 5 10 15
 Tyr Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys
 20 25 30
 Lys Glu Arg Phe Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe
 35 40 45
 Pro Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val
 50 55 60
 Phe Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met

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```

65          70          75          80
Lys Leu Leu Ser Lys Lys Asp Glu Ile Leu Ala Asn Phe Val Ala Gln
85          90          95
Val Thr Phe Ile Leu Ile Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser
100          105          110
Thr Leu Gly Val Gln Thr Thr Ser Ile Ile Thr Val Leu Gly Thr Val
115          120          125
Gly Ile Ala Val Ala Leu Ala Leu Lys Asp Tyr Leu Ser Ser Ile Ala
130          135          140
Gly Gly Ile Ile Leu Ile Ile Leu His Pro Phe Lys Lys Gly Asp Ile
145          150          155
Ile Glu Ile Ser Gly Leu Glu Gly Lys Val Glu Ala Leu Asn Phe Phe
165          170          175
Asn Thr Ser Leu Arg Leu His Asp Gly Arg Leu Ala Val Leu Pro Asn
180          185          190
Arg Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys
195          200          205
Arg Arg Ile Glu Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu
210          215          220
Leu Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Glu Lys Ile
225          230          235
Asp Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser
245          250          255
Ser Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile
260          265          270
Phe Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp
275          280          285
Ala Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn
290          295          300
Lys Gln Asp Ser Ser Lys
305          310

```

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895

```

Ser Lys Arg Thr Gln Gln Thr Phe Phe Leu Phe Ile Asp Glu Thr Lys
1          5          10          15
Asp Tyr Ile Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu
20          25          30
Ala Gln Ala Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys
35          40          45
Ile Ser Gln Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile
50          55          60
Gly Asn Leu Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu
65          70          75          80
Leu Ile Glu Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu
85          90          95

```

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```

His Asn Thr Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val
      100      105      110
Thr Asn Ala Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys
      115      120      125
Asn Tyr Phe Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser
      130      135      140
Met Ile Leu Lys Lys Gln Thr Lys Lys Leu Ile Arg Lys Ser Ile
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896

```

Leu Leu Lys Asn Ile Asp Glu Lys Lys Leu Ser Val Ser Lys Val Asn
1      5      10      15
Glu Lys Arg His Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys
      20      25      30
Cys Ala Phe Leu Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His
      35      40      45
Ser Lys Gly Leu His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro
      50      55      60
Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro
      65      70      75      80
Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr
      85      90      95
Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro
      100      105      110
Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp
      115      120      125
Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu
      130      135      140
Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile
145      150      155      160
Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu
      165      170      175
Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys
      180      185      190
Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu
      195      200      205
Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr
      210      215      220
Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly
225      230      235      240
Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe
      245      250      255
Thr Leu

```

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(2) INFORMATION FOR SEQ ID NO:1897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897

TATACCATGG TGGGCGCTAA

20

(2) INFORMATION FOR SEQ ID NO:1898:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898

ATGAATTCGA GTAAGGATTT TTG

23

(2) INFORMATION FOR SEQ ID NO:1899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900

TAGAATTTCGC ATAACGATCA ATC

23

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901

ATATCCATGG TGAGTTTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902

ATGAATTCAA TTTTATTT TGCCA

25

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903

AATTCCATGG TGGGGCTAT G

21

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904

ATGAATTCTC GATAGCCAAA ATC

23

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905

AATTCCATGG TGCATAACTT CCATT

25

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906

AAGAATTCTC TAGCATCCAA ATGGA

25

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907

ATTTCATGG TCATGTCTCA TATT

24

(2) INFORMATION FOR SEQ ID NO:1908:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908

ATGAATTCCA TCTTTTATTC CAC

23

(2) INFORMATION FOR SEQ ID NO:1909:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...27
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909

AACCATGGTG ATTTTAAGCA TTGAAAG

27

(2) INFORMATION FOR SEQ ID NO:1910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...28
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910

AAGAATTCCA CTCAAAATTT TTTAACAG

28

(2) INFORMATION FOR SEQ ID NO:1911:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911

GATCATCCAT ATGTTATCTT CTAAT

25

(2) INFORMATION FOR SEQ ID NO:1912:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912

TGAATTC AAC CATTTTAACC CTG

23

- (2) INFORMATION FOR SEQ ID NO::1913

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...27

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913

TATACCATGG TGAAATTTTT TCTTTTA

27

- (2) INFORMATION FOR SEQ ID NO:1914:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914

AGAATTCAAT TGGCTCTTGT AAAAG

25

- (2) INFORMATION FOR SEQ ID NO:1915:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

1429

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915

TATACCATGG TGATGGACAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916

ATGAATTCCC ACTTGGGGCG ATA

23

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917

TTATGGATCC AAACCAATTA AAAC

25

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918

TATCTCGAGT TATAGAGAAG GGC

23

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920

TAGAATTCGC CTCTAAACT TTAG

24

(2) INFORMATION FOR SEQ ID NO:1921:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921

TTAACCATCG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922

TAGAATTCGC ATAACGATCA ATC

23

1432

(2) INFORMATION FOR SEQ ID NO:1923:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923

ATATCCATGG TGAGTTTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:1924:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924

ATGAATTCAA TTTTATTATT TGCCA

25

(2) INFORMATION FOR SEQ ID NO:1925:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925

AATTCCATGG CTATCCAAAT CCG

23

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926

ATGAATTCGC CAAAATCGTA GTATT

25

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927

GATACCATGG AATTTATGAA AAAG

24

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928

TGAATTGGAA AAAGTGTAGT TATAC

25

(2) INFORMATION FOR SEQ ID NO::1929

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929

CCCTTCATT TAGAAATCG

19

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930

ATTTC AACCA ATTCAATGCG

20

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931

GCCCC TTTTG ATTGAAGCT

20

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932

TCGCTCCAAG ATACCAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1933

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933

CTTGAATTAG GGGCAAAGAT CG

22

(2) INFORMATION FOR SEQ ID NO:1934:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934

ATGCGTTTTT ACCCAAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1935:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935

ATAACGCCAC TTCCTTATTG GT

22

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(2) INFORMATION FOR SEQ ID NO:1936:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936

CTTTGGGTAA AAACGCATC

19

(2) INFORMATION FOR SEQ ID NO:1937:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937

CGATCTTTGA TCCTAATTCA

20

(2) INFORMATION FOR SEQ ID NO:1938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938

ATCAAGTTGC CTATGCTGA

19

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939

TTGAACACTT TTGATTATGC GG

22

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940

GGATTATGCG ATTGTTTTAC AAG

23

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

1439

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941

GTCTTTAGCA AAAATGGCGT C

21

(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942

AATGAGCGTA AGAGAGCCTT C

21

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

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(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943

CTTATGGGGG TATTGTCA

18

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944

AGCATGTGGG TATCCAGC

18

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945

AGGTTGTTGC CTAAAGACT

19

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946

CTGCCTCCAC CTTTGATC

18

(2) INFORMATION FOR SEQ ID NO:1947:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947

ACCAATATCA ATTGGCACT

19

(2) INFORMATION FOR SEQ ID NO:1948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948

ACTTGGA AAA GCTCTGCA

18

1442

(2) INFORMATION FOR SEQ ID NO:1949:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949

CTTGCTTGTC ATATCTAGC

19

(2) INFORMATION FOR SEQ ID NO:1950:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950

GTTGAAGTGT TGGTGCTA

18

(2) INFORMATION FOR SEQ ID NO:1951:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951

CAAGCAAGTG GTTTGGTTTT AG

22

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952

TGGAAAGAGC AAATCATTGA AG

22

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953

GCCCATAATC AAAAAGCCCA T

21

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

1444

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954

CTAAAACCAA ACCACTTGCT TGTC

24

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955

GTAAAACGAC GGCCAG

16

(2) INFORMATION FOR SEQ ID NO:1956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956

CAGGAAACAG CTATGAC

17

CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ

ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936,
 5 SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261,
 10 SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO: 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48,
 15 SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256, SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214, SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239, SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134, and SEQ ID NO: 330.

2. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID
 25 NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

3. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ
 35 ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO:

1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

4. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

5. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO:

- 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.
- 10 6. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.
7. A cell comprising a recombinant expression vector of claim 6.
- 15 8. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 7 under conditions that permit expression of the polypeptide.
9. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO:

- 1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO: 1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986.

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SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

10. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

11. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

12. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217,

SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

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13. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

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14. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

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15. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

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16. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

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17. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087,

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SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

18. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

19. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

20. A recombinant expression vector comprising the nucleic acid of claim 9 operably linked to a transcription regulatory element.

21. A cell comprising a recombinant expression vector of claim 20.

22. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 21 under conditions that permit expression of the polypeptide.

23. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID

NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411,
 SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID
 NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203,
 SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO:
 5 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ
 ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO:
 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ
 ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO:
 10 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ
 ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO:
 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ
 ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ
 ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ
 ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ
 15 ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ
 ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219,
 SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO:
 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO:
 20 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO:
 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID
 NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ ID NO: 17, SEQ ID
 NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID
 NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID
 NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ
 25 ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212,
 SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237,
 SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276,
 SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO:
 30 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID
 NO: 171.

24. A recombinant expression vector comprising the nucleic acid of claim 23 operably linked to a transcription regulatory element.

35 25. A cell comprising a recombinant expression vector of claim 24.

26. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 25 under conditions that permit expression of the polypeptide.

27. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

28. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO:

116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

5 29. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ
10 ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID
15 NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

 30. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment
20 thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

25 31. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO:
30 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

35 32. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO:
40 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

33. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions encoded by the nucleic acid selected
5 from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, and SEQ ID NO: 264.

34. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or
10 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ
15 ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

35. A recombinant expression vector comprising the nucleic acid of claim 27 operably linked to a transcription regulatory element.

20 36. A cell comprising a recombinant expression vector of claim 35.

37. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 36 under conditions that permit expression of the polypeptide.

25 38. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 1.

39. A vaccine composition of claim 38, further comprising a pharmaceutically acceptable carrier.
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40. A vaccine composition of claim 39, wherein the pharmaceutically acceptable carrier is an adjuvant.

41. A method of treating a subject for *H. pylori* infection comprising
35 administering to a subject a vaccine composition of claim 38, such that treatment of *H. pylori* infection occurs.

42. A method of claim 41, wherein the treatment is a prophylactic treatment.
40

43. A method of claim 41, wherein the treatment is a therapeutic treatment.
44. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 9.
- 5 45. A vaccine composition of claim 44, further comprising a pharmaceutically acceptable carrier.
- 10 46. A vaccine composition of claim 45, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 15 47. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 44, such that treatment of *H. pylori* infection occurs.
48. A method of claim 47, wherein the treatment is a prophylactic treatment.
49. A method of claim 47, wherein the treatment is a therapeutic treatment.
- 20 50. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 23.
- 25 51. A vaccine composition of claim 50, further comprising a pharmaceutically acceptable carrier.
52. A vaccine composition of claim 51, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 30 53. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 50, such that treatment of *H. pylori* infection occurs.
- 35 54. A method of claim 53, wherein the treatment is a prophylactic treatment.
55. A method of claim 53, wherein the treatment is a therapeutic treatment.

56. A purified *H. pylori* cell envelope polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO:

809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO: 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

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57. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

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58. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611. SEQ

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ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

59. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, and SEQ ID NO: 765.

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60. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO:

1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 5 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

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61. A purified *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 15 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 25 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 30 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488, SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 35 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ

ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID NO: 1828, SEQ ID NO:
1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839, SEQ ID NO: 1852, SEQ
ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO:
1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ
5 ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO:
1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508, SEQ ID NO: 1541, SEQ
ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO:
1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ
ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO:
10 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ
ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID NO: 1787, SEQ ID NO:
1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ
ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678,
SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO:
15 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID
NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ
ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562,
SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO:
861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID
20 NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ
ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429,
SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO:
822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID
NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ
25 ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415,
SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO:
399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID
NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ
ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832,
30 SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO:
393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ ID NO: 458, SEQ ID
NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ
ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492,
SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID NO: 426, SEQ ID NO:
35 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID
NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ
ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618,
SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID NO: 785, SEQ ID NO:
457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID

NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

62. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678.

63. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733.

64. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

65. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

66. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

67. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

68. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

69. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

70. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis selected from the group consisting of
5 SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

71. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic
10 polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

72. A purified *H. pylori* secreted or periplasmic polypeptide or a fragment
15 thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO:
20 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ
25 ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO:
30 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID
35 NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ

ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

73. A purified *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID

NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

74. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

75. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

76. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

77. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting

of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, and SEQ ID NO: 571.

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78. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 409.

79. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

80. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

81. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 56.

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82. A vaccine composition of claim 81, further comprising a pharmaceutically acceptable carrier.

83. A vaccine composition of claim 82, wherein the pharmaceutically acceptable carrier is an adjuvant.

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84. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 81, such that treatment of *H. pylori*

infection occurs.

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85. A method of claim 84, wherein the treatment is a prophylactic treatment.
86. A method of claim 84, wherein the treatment is a therapeutic treatment.
- 5 87. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 61.
- 10 88. A vaccine composition of claim 87, further comprising a pharmaceutically acceptable carrier.
89. A vaccine composition of claim 88, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 15 90. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 87, such that treatment of *H. pylori* infection occurs.
- 20 91. A method of claim 90, wherein the treatment is a prophylactic treatment.
92. A method of claim 90, wherein the treatment is a therapeutic treatment.
- 25 93. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 72.
94. A vaccine composition of claim 93, further comprising a pharmaceutically acceptable carrier.
- 30 95. A vaccine composition of claim 94, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 35 96. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 93, such that treatment of *H. pylori* infection occurs.
97. A method of claim 96, wherein the treatment is a prophylactic treatment.

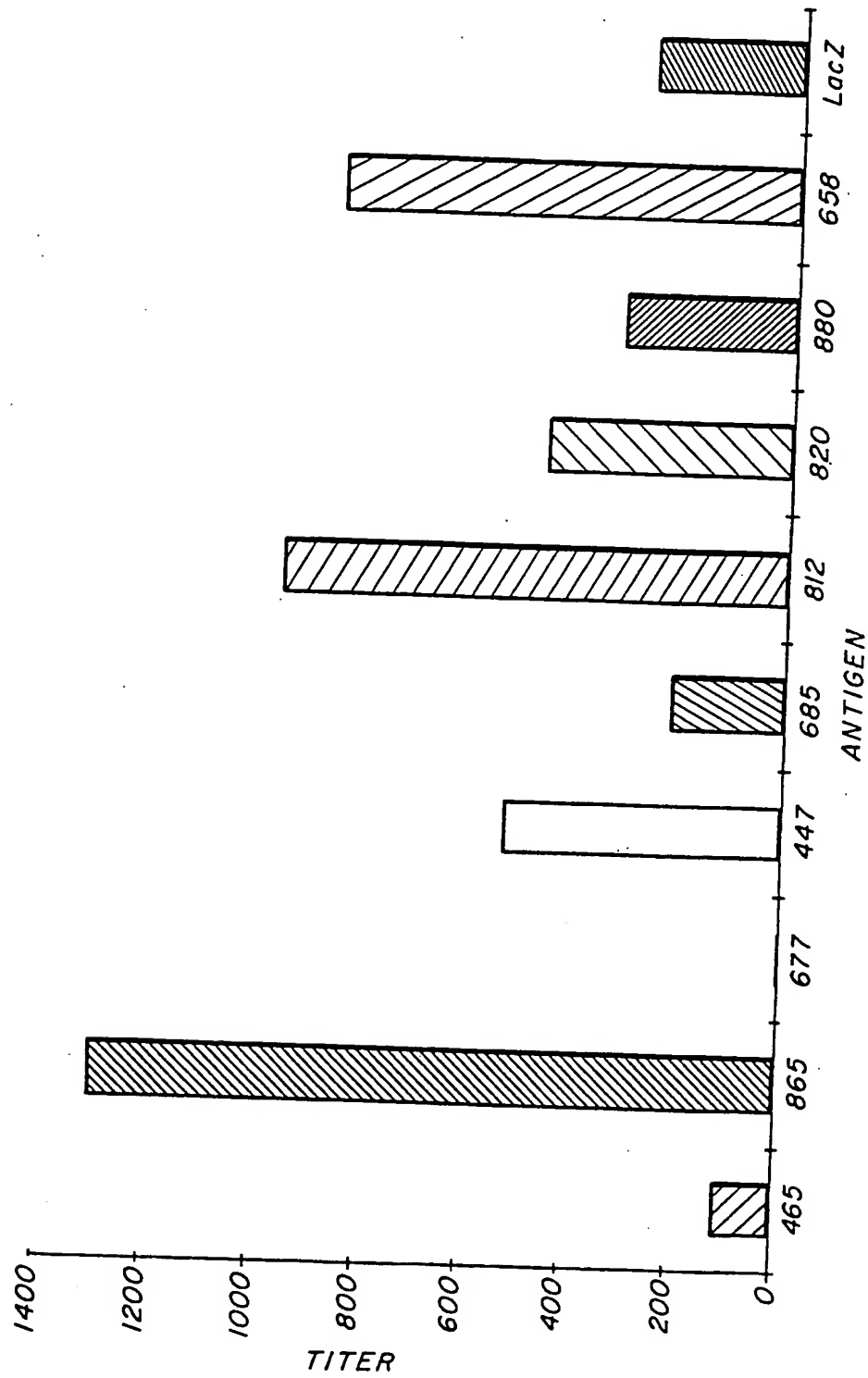
98. A method of claim 96, wherein the treatment is a therapeutic treatment.
99. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 73.
- 5 100. A vaccine composition of claim 99, further comprising a pharmaceutically acceptable carrier.
- 10 101. A vaccine composition of claim 100, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 15 102. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 99, such that treatment of *H. pylori* infection occurs.
103. A method of claim 102, wherein the treatment is a prophylactic treatment.
104. A method of claim 102, wherein the treatment is a therapeutic treatment.
- 20 105. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:
- (a) contacting a sample with a nucleic acid of claim 1 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- 25 (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.
106. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:
- 30 (a) contacting a sample with a nucleic acid of claim 9 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid
- 35 indicates the presence of a *Helicobacter* nucleic acid in the sample.
107. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

- (a) contacting a sample with a nucleic acid of claim 23 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid
- 5 indicates the presence of a *Helicobacter* nucleic acid in the sample.

108. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

- (a) contacting a sample with a nucleic acid of claim 27 under conditions
- 10 in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

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**FIG. 1**

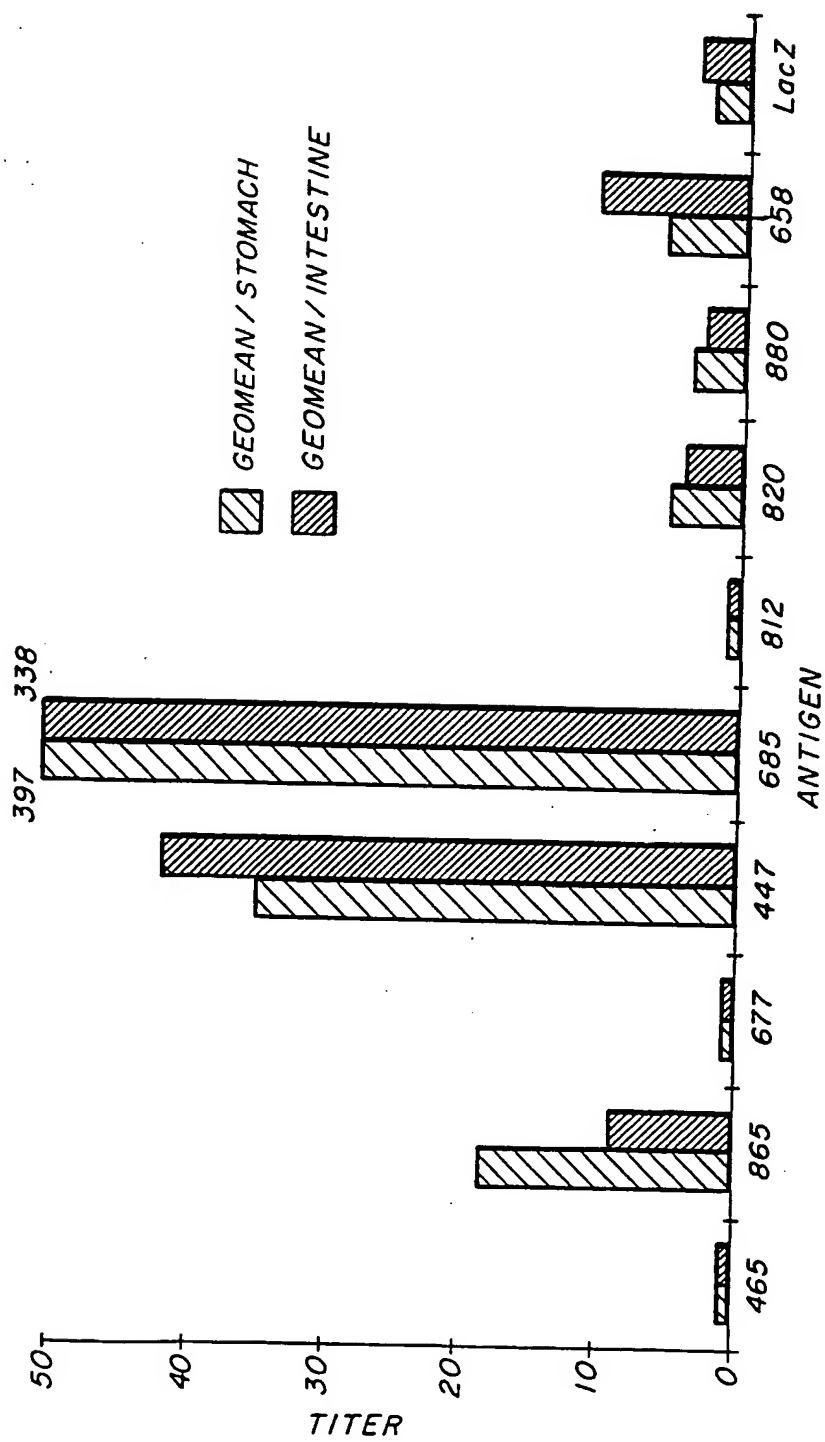


FIG. 2



FIG. 3

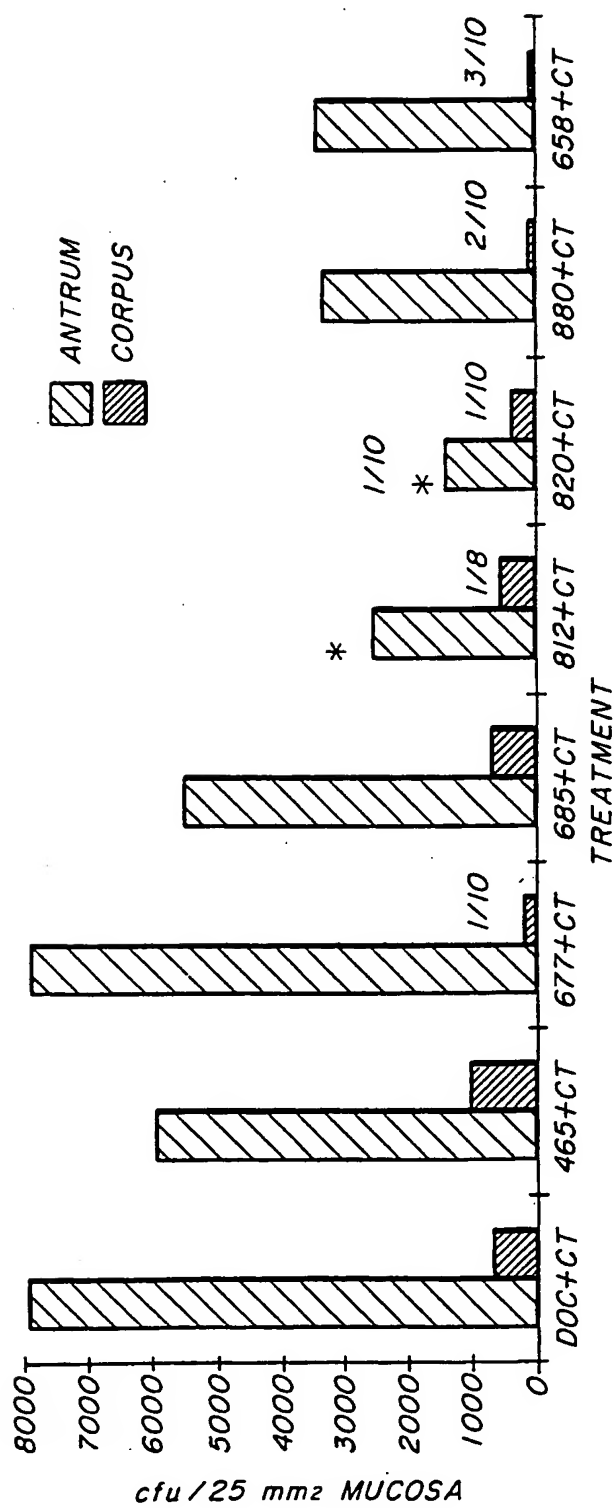


FIG. 4

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US96/09122

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 15/00

US CL : 514/44

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/44; 435/172.3; 935/6, 9, 11

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Helicobacter pylori reading file of authorized officer.Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EMBL/GENEBANK, DIALOG, MEDLINE
search terms: Helicobacter pylori, gene?

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|---|-----------------------|
| Y | BUKANOV et al. Ordered cosmid library and high-resolution physical-genetic map of Helicobacter pylori strain NCTC11638. Molecular Microbiology. February 1994, Vol. 11, No. 3, pages 509-523, especially experimental procedures section pages 519-521. | 1, 5, 56, 60 |
| Y | TAYLOR et al. Construction of a Helicobacter pylori genome map and demonstration of diversity at the genome level. Journal of Bacteriology. November 1992, Vol. 174, No. 21, pages 6800-6806, especially pages 6800-6801. | 1, 5, 56, 60 |

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

| | | |
|--|------|--|
| * Special categories of cited documents: | * T | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| * A* document defining the general state of the art which is not considered to be of particular relevance | * X* | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| * E* earlier document published on or after the international filing date | * Y* | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| * L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | * A* | document member of the same patent family |
| * O* document referring to an oral disclosure, use, exhibition or other means | | |
| * P* document published prior to the international filing date but later than the priority date claimed | | |

Date of the actual completion of the international search

11 SEPTEMBER 1996

Date of mailing of the international search report

23.09.1996

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/09122

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1, 5, 56 and 60

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This International Search Authority has found 263 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined the appropriate additional examination fees must be paid.

The species are as follows:

Group I contains a separate DNA species for each sequence mentioned. Therefore, there is a minimum of 527 species.

Group II contains at least one polypeptide for each DNA sequence mentioned. Therefore is a minimum of 527 species in this Group.

For the species in each Group that applicant elects, a total of 10(ten) specified sequences will be searched and no more than 4(FOUR) specified sequences will be searched for each additional fee paid.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2 the species lack the same or corresponding special technical features for the following reasons: There is no relationship between or among the various nucleotide and amino acid sequences mentioned in the claims.

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